## STIC-Biotech/ChemLib

Q 160624

From:

Sent:

Ibrahim, Medina A. Tuesday, July 26, 2005 6:18 PM STIC-Biotech/ChemLib

To:

Subject:

09/765, 555

Please search the following:

Please search the following:

1. DNA encoding SEQ ID NO: 14- 18. Thanks

Medina A. Ibrahim Patent Examiner, GAU-1638 transgenic plants and plant breeding Remsen-2B07 mailbox-2C18 (571) 272-0797

STAFF USE ONLY

Searcher: Searcher Phone: 2-Date Searcher Picked Date Completed: Searcher Prep/Rev. Time: Online Time:

Type of Search Interference: SPDI: S/L:\_ Oligomer:\_ Encode/Transl: Structure#: Text: Inventor:\_\_\_\_ Litigation:\_

Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM: www/Internet: Other(Specify):\_

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HH04B08u DKFZp586H DKFZp434J

CB862524 BAL048427 BAL042909 B

CARRIDAY KOD94C10ALO38B11 DKFZp5660
CAB80032 BD156F05CAB86082 BD154F04ALO44407 DKFZp434D
CA895436 BD192AD7ALO39076 DKFZp566C
CK39437 PGGABA2H
ALO39076 DKFZp566C
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CB62715 HG03P14u
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ALO39589 DKFZp434G
CA887583 BDKFZp566K
ALO39649 DKFZp434G
CA887583 BWFZp5434G
CA887583 HO44K05w

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Run on:

Title:

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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.

I (bases 1 to 794)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
BSTS from mycelia of Colletotrichum trifolii race 1
L Unpublished (2002)
Other ESTS: EST61249
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TICR sequence name: MTSAH6/TV More information is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ751936 794 bp mRNA linear EST 18-JUL-2002 EST632499 DSCT Colletotrichum trifolii cDNA clone pDSCT8-67, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="pDSCT8-67"
/tissue_type="mycelia"
/tissue_type="mycelia"
/dev stage="Young, actively growing mycelia (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%glucose)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.medicago.org
Seq primer: (grA Ath CgA CtC ACt Ath ggg C).
Location/Qualifiers
1.794
/organism="Colletotrichum trifolii"
/mol type="mRNA"
/strāin="race 1"
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DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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AUTHORS
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    BQ751936 EST632499
CK334523 haggadadD0
CK118014 218n06.pl
BQ751655 EST632218
BQ751220 EST631783
CB863541 HHO4A08Y
AL038548 DKFZpS66E
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                              34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          nucleic search, using sw model
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AY080106
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seq length: 200000000
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Match Length DB
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9b est2:

9b htc:

9b est4:

9b est6:

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Maximum DB
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Result

seguence

mRNA

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E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after ECORI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DHSalpha which were plated onto medium with X-gal for selection of recombinants."
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                                                                                                                                                            GACACTTTCGAATGGCGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGT
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23.6%; Score 778; DB 5; Length 794;
al Similarity 98.7%; Pred. No. 1.3e-217;
784; Conservative 0; Mismatches 10; Indels
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Eukaryota, Metazoa, Nematoda, Chromadorea, Tylenchina,
Tylenchoidea, Heteroderidae, Heteroderinae, Heterodera.
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                                                                                                             E 1 (Dases 1 to 779)
S Wang,X., Allen,R., Gao,B., Goellner,M., Maier,T., Baum,T.,
Hussey,R. and Davis,E.
Submission: Wang, Allen, Gao, Goellner, Maier, Baum, Hussey, Davis
L Unpublished (2003)
Contact: Tom Maier
Department of Plant Pathology, Baum Lab
Iowa State University
351 Bessey Hall, Ames, IA 50011, USA
Tel: 515-294-8854
Fax: 515-294-6420
Email: trmaier@iastate.edu
Heterodera glycines Gland Cell Amplified cDNA Library, single par
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                                                                                                                                                                                                                                                                                                                                                                           /organism="Heterodera glycines"
/mol_type="mRNA"
/db_xref="taxon:51029"
/cell_type="mlxed parasitic juvenile"
/dev_stage="mlxed parasitic juvenile"
/clone_lib="Gland Cell Amplified cDNA Library"
/note="Organ: gland cell; Vector: pSportII"
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Pred. No. 2e-215;
0; Mismatches 5; Indels
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   CK394523
CK394523.1 GI:40389794
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Best Local Similarity 99.4%;
Matches ,773; Conservative
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ACCESSION
VERSION
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JOURNAL
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AUTHORS
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BQ751655 100-2002 T93 bp mRNA linear EST 18-JUL-2002 EST632218 DSCT Colletotrichum trifolii cDNA clone pDSCT6-59, mRNA ACCGCTGCTGCAGACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCT 1044 1104 ö 360 240 420 540 984 900 999 504 564 180 624 300 744 804 864 480 924 9 Colletotrichum trifolii
Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.

1 (bases 1 to 793)
Samac,D.A. Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,
Cheung,F. and Fraser,C.M.
ESTS from mycelia of Colletotrichum trifolii race 1
Unpublished (2002) 301 ATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTG 865 TGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTT 121 ATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTTTCT 361 CCATGTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGGATCGTTCCCACTGGGA 805 TGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGGCGCCATTACCGAGTCCGGGC TGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCATTACCGAGTCCGGGC ATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCAGCGTGG 641 ATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCAGCGTGG 601 ACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCT CACTGGTGAAAAGAAAAACCACCCTGGCGCCCCAATACGCAAAACCGCCTCTCCCCGCGCGT 661 CACTGGTGAAAAGAAAAACCACCCTGGCGCCCAATACGCAAAACCGCCTCTCCCCGCGCGT 385 GCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGC GCGGCGTCGAAAGCCTGTAAAAGCGGCGGTGCACCAATCTTCTCGCGCAAACGCGTCAGTGGGC **ATGITCCGCCGITATITCTTGATGTCTCTGACCAGACACCCCATCAACAGTATTATTTTCT** CCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAA **ATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTG** CCATGTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGA Gaps ö TGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAA 1152 721 TGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAA 768 Indels ö Mismatches . 0 BQ751655 BQ751655.1 GI:21907060 Conservative sequence. 768; 265 ( 685 925 1105 505 745 985 1045 61 625 421 SOURCE ORGANISM DEFINITION ACCESSION VERSION KEYWORDS REFERENCE AUTHORS TITLE JOURNAL Matches RESULT 4 BQ751655

662

722

782

542

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ENKARYOCA: Pungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes; Bungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae; Colletotrichum.

1 (bases 1 to 806)

2 Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T., Cheung,F. and Fraser,C.M.

ETS from mycelia of Colletotrichum trifolii race 1

Unpublished (2002)

Unpublished (2002)

Contact: Deborah A. Samac

Department of Plant Pathology

University of Minnesota

495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

Tel: 615 649 5058
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/lab_host="DHSalpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BQ751220
806 bp mRNA linear EST 18-JUL-2002
EST631783 DSCT Colletotrichum trifolii cDNA clone pDSCT3-64, mRNA
                                                                                                                                                                         GAACGGBAAGGCGACTGGAGTGCCATGTCCGGTTTTCA--CAAACATGCAAATGCTGAAT 778
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/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtll from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
                     GCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA
                                                                             GCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA
                                                                                                                                       CCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAACTCTG
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TIGR sequence name: MTSAC64TV More information is available at:

    .806
    /organism="Colletotrichum trifolii"

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Seg primer: (gtA AtA CgA CtC ACt AtA ggg
Location/Qualifiers
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clone="pDSCT3-64"
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/strain="race 1"
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BQ751220.1 GI:21906625
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Colletotrichum trifolii
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//clone_libe_DSCT.
//clone_libe_D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="mycelia"
/dev stage="Young, actively growing mycelia (3 days after incoulation) grown in liquid culture (cutin minimal medium containing 2*glucose)."
/lab_host="DH5alpha"
                                                                                                                                    55108, USA
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                     Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 5510
Tel: 612 625 1243
Fax: 614 649 5058
Email: debbys@puccini.crl.umn.edu
TICR sequence name: MTSAFS9TV More information is available.
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    .793
    /organism="Colletotrichum trifolii"

                                                                                                                                                                                                                                                                                              Seq primer: (gtÅ AtA CgA CtC ACt AtA ggg C)
Location/Qualifiers
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clone="pDSCT6-59"
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/strain="race 1"
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   Other_ESTs: EST632217
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lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of
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                                                                                 22.9%; Score 755.4; DB 5; larity 97.4%; Pred. No. 6.3e-211; Conservative 0; Mismatches 16;
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CB863541 689 bp mRNA linear EST 22-APR-2003 HH04A08y HH Hordeum vulgare cDNA clone HH04A08 3-PRIME, mRNA sequence.

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Hordeum vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Hordeum.
1 (bases 1 to 689)
Varshney, R. K., Zhang, H., Burton, R., Stein, N., Langridge, P. and
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/note="weetcr: pSPORT; Site_1: Sall (5-end of cDNA);
Site_2: Not! (3-end of cDNA); Due to the cloning system
used blue/white selection for recombinants is not 100 %
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Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5595
Email: stein@ipk-gatersleben.de
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/mol_type="mRNA"
/cultivar="Sloop"
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/dev_stage="coleoptile, 1
/lab_host="DH108"
                                                                                                                                               Graner, A.
Barley ESTs from coleoptile tissue
Unpublished (2003)
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/db_xref="taxon:4513"
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                                                                                          212 GCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTGAT 271
                                                                                                                                                                  331 AATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGGTGGTAGAACGAAGCGGGG 390
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                                                         AACCAGGCCAGCCACGTTTCTGCGAAAACGCGGG-AAAAAGTGGAAGCGGCGATGGCGGA
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Email: forest@sunstroke.sdsu.edu
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DKPZp566E0346_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKRZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
eveloping consortium of the German Genome Project. No s1 sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
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This clone (DKF2p566E0346) is available at the R2PD in Berlin.
Please contact the R2PD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
209 ACTAATGTTCCGGCGTTATTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATT
                                                                                                            561 TICTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAG
                                                      ACTAATGTTCCGGCGTTATTTCTTGATGTCTCGACCAGACACCCCATCAACAGTATTATT
                                                                                                                                                                                         89 CAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCGTCTGGGTGGC
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20.5%; Score 676.4; DB 1;
Best Local Similarity 99.6%; Pred. No. 1.3e-187;
Matches 699; Conservative 0; Mismatches 1;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp566E0346"
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Unpublished (1999)
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EST (Otten:
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GSS 06-NOV-2002
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I (Dases 1 to 710)

Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Mead, D., Azam, F. and Rohwer, F.

Benomic analysis of uncultured marine viral communities
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
AY080106 Aripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3G6L, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biology Dept.
San Diego State University
5500 Campanile Dr. San Diego, CA 92102,
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659; Conservative
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                                                            fincte="Marine viruses were isolated from 200 liters of surface seavater using a combination of differential filtration and density-dependent gradient centrifugation. Linker-amplified shotgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating dsDNA linkers to the ends, and amplifying the fragments using Vent DNA polymerase. The resulting fragments were ligated into the pSMART vector and electroporated into MC12 cells (Lucigen; Middleton,
                                                                                                                                                                                                                                                                                               67
                          /clone="81051p3G6L"
/clone_lib="Scripps Pier (La Jolla, CA) uncultured virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGACTGGGCGGGGGCATCTGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGG
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                                                                                                                                                                                                                   20.5%; Score 676; DB 8; I 98.9%; Pred. No. 1.7e-187; iive 0; Mismatches 7;
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 type="genomic DNA"
xref="taxon:186617"
                                                 community"
                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.9
Matches 690; Conservative
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                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
mamalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
Ansorge,W., Benes,V., Krieger,S., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No r1 sequence available.
This clone (DKRZp4341102) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev stage="adult"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
DKFZp4341102_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp4341102_3', mRNA sequence.
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99.7%; Pred. No. 4.5e-179;
ive 0; Mismatches 1;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="taxon:9606"
/clone="DKPZp4141102"
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Unpublished (1999)
Contact: MIPS
                                                                                  AL044483.1 GI:5432701
EST.
                                                                                                                                       Homo sapiens (human)
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ATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTTCT 564

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CB863814 62-2003
HH07B20y HH Hordeum vulgare cDNA clone HH07B20 3-PRIME, mRNA
          270 ATTGGCGTIGCCACCTCCAGTCTGGCCCTGCACGCGCCGTCGCAAATTGTCGCGGCGATT 329
                                                                                                                                                                                                                                                                        449
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Hordeum vulgare
Hordeum vulgare
Eukaryots, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
I (bases 1 to 624)
Varshney, R.K., Zhang, H., Burton, R., Stein, N., Langridge, P. and
                                                             210 GAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTG
                                                                                                                                                  330 AAAICICGCGCCGAICAACIGGGIGCCAGCGIGGIGGIGGIGGIAGAAGCGAAGCGGC
                                                                                                                                                                                                                                                               GTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101 GAAGACGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAATCGCG
                                                                                                                                                                                                                                                                                                                                   Barley, ESTE from coleoptile tissue
Unpublished (2003)
Contact. Stein Nilo
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensestr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTTAGCGGGCCCATTAAGTTCTGTCTGGGCGCGTCTGCG 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 CTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCG 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: stein@ipk-gatersleben.de
Insert Length: 624 Std Error: 0.00
Plate: 7 row: B column: 20

    .624
    /organism="Hordeum vulgare"

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/cultivar="6loop"
/db_xref="6AB1:555471"
/db_xref="6AB1:55471"
/db_xref="taxon:4513"
/clone="HH07B20"
/ti88ue_type="coleoptile"
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CB863814.1 GI:30058373
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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JOURNAL
COMMENT
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624
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                                                                                                                                                                                   685 ATAAAIAICTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTG 744
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                                                                                                                                       GTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACCGTTTCCCCGCGTG 149
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                                                                                                                                                                                                        61 ATAMATATCTCACTCGCAATCAACTTCAGCGGAAAGGGGAAAGGGACTGGAGTG 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachis, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus, Xenopus.

[1] (bases 1 to 641)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
                                                   CCCATGAAGACGGTACGCGACTGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAA
                                                                                                                  CGCGGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAAACCA
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dev stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Ill Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-01-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
Xenopus laevis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL077k02"
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Location/Qualifiers
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EST.
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CCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTG 602
/dev_stage="coleoptile, 1 day old"
/lab host="DH108"
/clome lib="HH"
/note="Vector: pSPORT; Site_1: SalI (5-end of cDNA);
Site_2: NotI (3-end of cDNA); Due to the cloning system used blue/white selection for recombinants is not 100 % reliable. Average insert size is 1.3 kb."
                                                                                                                                                                                                                                                                                                                                              439 CGGGAAAAAGGGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 GCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTG
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                                                                                                                                               Query Match 18.7%; Score 615.8; DB 6; Length 624; Best Local Similarity 99.7%; Pred. No. 9.5e-170; Matches 617; Conservative 0; Mismatches 2; Indels 0.
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AL045353
DKFZp4348D75_81 434 (synonym: htes3) Homo sapiens cDNA clone
DKTZp4348D75_3', mRNA sequence.
                                                       AL045353
AL045353.1 GI:5433506
                                                                                                 sapiens (human)
                                                                                                               Homo sapiens
                                                                                                  Ношо
AL045353/c
LOCUS
DEFINITION
                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
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REFERENCE AUTHORS

196 376 1049 1109 256 1169 g q g 임 ₹ ò ò Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 794)
Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); sequenced by Qiagen within the cDNA
sequencing consortium of the German Genome Project. rl sequence
also available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. /mol\_type="mRNN"
/mol\_type="mRNN"
/db xref="taxon:966"
/clone="bype="taxon:966"
/tissue\_type="testis"
/dev\_stage="adult"
/dev\_stage="adult"
/clone lin="44 (synonym: htes3)"
/clone lin="44 (synonym: htes3)" 1. .794 /organism="Homo sapiens" et al.) EST (Duesterhoeft, Unpublished (1999) Contact: MIPS MIPS TITLE JOURNAL COMMENT FEATURES

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Gaps

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560 122 500 182 440 242 380 302 320 362 260 422 200 482

62

Gaps 2 Length 794; Query Match 18.5%; Score 612; DB 1; Length 79 Best Local Similarity 99.7%; Pred. No. 1.4e-168; Matches 634; Conservative 0; Mismatches 0; Indels

7 628 736 688 677 748 617 808 557 TGAAGACGGTACGCGACTGGGCGTGGAG-ATCTGGTCGCATTGGGTCACCAGCAAATGGC GCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGGGTCTG-GTCTGGCTGGCTGGCATAA GTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGGCATCGTTCCCACTGCGATGCT TGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATCGC ATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAAACGGGAAGGCGACTGGAGTGCCAT 676 ATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTGCCAT GTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCT 919 794 735 689 749 569 629 셤 임 셤 g ò à ò ò

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CTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACT 1048 317 377 868 497 928 437 988 436 ccccccrraaccaccarcaacaggarrrccccrccrcccaaaccagccrcc CGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTATAT cerrecreatarcrestracresaraceacaraceacaasacacacaretrarar CCCGCCGTTAACCACCATCAAACAGGATTTTTCGCCTGCTGGGGCAAACCAGCGTGGACCG 496 869 929 989 g ò g g ò ò ò

CGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCA 1168 GGTGAAAAGAAAACCACCCTGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGC 1108 316 GGTGAAAAGAAAAACCCCCTGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGC CGATTCATTAATGCAGCTGGCACGACGAGTTTCCCGACTGGAAGCGGAGTGAGAGCA

257

197

ACGCAATTAATGTGAGTTAGCTCACTCATTAGGCAC 1204 ACGCAATTAATGTGAGTTAGCTCACTCATTAGGCAC 161

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2534 AGAIGICCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGCGGTCGTC 2593
2414 AAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATC 2473
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                          272 CACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCGC 213
                                                                                                                                                                                                                  212 AGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCCGCCAGGGGTCGTC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface seawater using a combination of differential filtration and density-dependent gradient centrifugation. Linker-amplified shotgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating dsDNA linkers to the ends, and amplifying the fragments using Vent DNA polymerase. The resulting fragments were ligated into the pSMART vector and electroporated into MC12 cells (Lucigen; Middleton, WI)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Mead, D., Azam, F. and Rohwer, F.
Mead, D., Azam, F. and Rohwer, F.
Mead, D., Azam, F. and Rohwer, F.
Proc. Matl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
22294988
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/clone lib="Scripps Pier (La Jolla, CA) uncultured virus
community"
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/organism="uncultured marine virus"
/mol_type="genomic_DNA"
/db_xref="taxon:186617"
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Biology Dept.
San Diego State University
5500 Campanile Dr, San Diego, CA 92102, USA
Tel: 6195941336
                                                                                                                                                                                                                                                                               2594 AGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT 2628
                                                                                                                                                                                                                                                                                                         152 AGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; environmental samples.
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Location/Qualifiers
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Email: forest@s
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PRI0124a_C01 - PRI0124a_B21 (752) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic cL655575
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Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
AppabB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996 TTCACCTGGCCGCTGATTGCTGCTGAC-GGGGGTTATGCGTTCAAGTATGAAAACGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     752 TTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAGTATGAAACGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-19, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommeretuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and egequenced at Vancouver, Canada.
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llarity 98.9%; Pred. No. 6e-166;
Conservative 0; Mismatches 5; Indels

    .752
    .752mism="Pristionchus pacificus"
/mol type="genomic DNA"
/strain="California"

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Class: fosmid ends.
Location/Qualifiers
                                                                                                                                                                    CL655575.1 GI:50134897
GSS.
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Pristionchus pacificus
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email 8.wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd.,
Braunschweig/Germany) within the cDNA sequencing consortium of the
German Genome Project.
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1 (Bases 1 to 589)
Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. and
406
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This clone (DKRZp564C157) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                    GGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCGCTGGA
                                                                                                                                                                                                                                                                            CATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGAT
                                                                                                                          TGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCACTAATGTTCCAGCGTTATTTCTTGA
                                                                                                                                                                               CATGCAAATGCTGAATGAGGGCATCCTTCCCACTGCGATGCTGGTTGCCAACGATCAGAT
           TGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGA
                                                                                                                                                                 TGTCTCTGACCAGACCCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACT
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ACTGGGTGCCAGCGTGGTGGTGCTAGAACGAAGCGGCGTCGAAGCCTGTAAAGC
                                                    GCCGTGCACATCTTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKFZps64C157_r1 564 (synonym: hfbr2) Homo sapiens CDNA clone AL037742
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/db_xref="taxon:9606"
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Unpublished (1999)
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Homo sapiens
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/dev_stage="fetal"
/lab_host="X1-2blue"
/clone_lib="564 (synonym: hfbr2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAAACCACCCTGGCGCCCCAATACGCAAACCGCCTCTCCCCCGCGCGTT 1105
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                                                                                                                                     DB 1;
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Pred. No. 4.5e-161;
0; Mismatches 2;
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Perfect score:

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                             US-10-263-153-40
US-10-263-153-40
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US-10-263-153-10
US-10-263-133-10
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US-10-671-995A-1
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Publication No. US20030037355A1
SEQUENCE 16, Application US/09765555
Publication No. US20030037355A1
SEQUENCE 17 PERMITTON:
APPLICANT: THE SCRIPPS Research Institute
TITLE OF INVENTION: Expression in plants
FILE PEPERENCE: 27801-20014.40
CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 60/177,468
PRIOR FILING DATE: 2000-01-21
PRIOR PRING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 16
LENGTH: 3300
TYPE: DNA
CREANISM: Artificial Sequence
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US-10-420-034A-32
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100.0%; Score 3300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3300; Conservative 0; Mismatches
                                 US-09-765-555-16
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   Sequence 18, Appl
Sequence 14, Appl
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Sequence 1, Appli
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                                                                                                           Search time 1309.2 Seconds (without alignments) 16314.373 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-765-555-14
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US-09-765-555-17
US-09-765-555-17
US-08-257-184A-1
US-10-257-184A-1
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                                                                                                                                                                                                                                                                                     7287783 segs, 3236178273 residues
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                                                                                                             2, 2005, 10:29:49;
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Maximum Match 100%
Listing first 45 summaries
                                                                               nucleic search, using sw model
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Score

Result 80.

Sequence 137, App Sequence 54, Appl Sequence 2, Appli Sequence 1, Appli

Sequence 54, Appli Sequence 2, Appli Sequence 1, Appli Sequence 3, Appli Sequence 4, Appli Sequence 30, Appli

GENERAL INFORMA Sequence 1, Appli Sequence 2, Appli Sequence 19, Appl

Sequence 1, Appli Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 2, Appli

Sequence 3, Appl Sequence 52, App Sequence 52, App Sequence 2, Appl

Sequence 30, Appl Sequence 25, Appl Sequence 20, Appl Sequence 61, Appl Sequence 61, Appl Sequence 71, Appl Sequence 15, Appl Sequence 19, Appl Sequence 194, Appl

Db 1081 CGCAACCCCTCTCCCCGCGTTGGCCATTCATTAATGCAGCTGGCACGACAGGTTT 11	OY         1141         CCCGACTGGAAAGCGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA	QY 1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG 1260	QY 1261 TCAGGCACCATCGGAAGCTGTGGCTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 132	QY         1321         TGTCGCTCAAGGGGACTCCCGTTCTGGATAATGTTTTTGCGCCGACATCATAACGGTT         138	QY 1381 CTGGCAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGGG 144	OY 1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCGGTCCGTTTAGGTGTTTTGACGA 1500  Db 1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500	QY     1501     GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGGAAACTGGTAATCTGG     1501       DD	Oy 1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAATTCGAGAAAGGT 162	QV         1621         ACCGGAATTAAAGTCACCGTTGAGCATCGGATAAACTGGAAGAGAAATTCCCACAGGTT         168           DD         1621         ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT         168	QY         1681         GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTACTACTACTACTGGGCACACTACGTGGCCAACTGGCCAACTGGCCAACTGGCCAACTGGCCAACTGACACGACGCAACTGGCGATGGCCCTCAACATTATCTTCTGGGCACACGACGCTTTGGTGGCTAC         174	QY         1741 GCTCAATCTGGCTGAAATCACCCCGGACAAAGGTTCCAGGACAAGCTGTAT 1800           DD         1741 GCTCAATCTGGCTGAAATCACCCCGGACAAAGGTTCCAGGACAAGCTGTAT 1800	QY 1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860	OY 1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920  DD 1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCGGCCAAAAACCTGGGAA 1920	OY 1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGGCGCGCTGATGTTCAAC 1980	Qy         1981         CTGCAAGAACCGIACTTCACCTGGCCGCTGATTGCTGACGGGGGTTATGCGTTCAAG         2040           Db         1981         CTGCAAGAACCGIACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG         2040	OY 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGGTGGATAAGGCTGGGGGAAAGGG 2100	OY 2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC 2160	Oy 2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220
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                                                                                                                                                                                       APPLICANT: The Scripps Research Institute
TITLE OF INVENTION: Methods and compositions to modulate;
TITLE OF INVENTION: expression in plants
FILE REPRENCE: 27801-20014.40
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 09/620,897
PRIOR APPLICATION NUMBER: US 09/620,897
PRIOR PLILING DATE: 2000-01-21
PRIOR PELING DATE: 2000-01-21
PRIOR PELING DATE: 2000-01-21
SPRIOR PRIOR DATE: 2000-01-21
SPRIOR FILING DATE: 2000-01-21
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                                                                             US-09-765-555-18

"Sequence 18, Application US/09765555; Publication No. US20030037355A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Simi
Matches 3248;
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ACGGGTGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGCACCAGCGGCTCC	3241 ACCGGTAAAAAACTAGTGGCCAGGCCAGTACCCGTACCAGACTTCCGGACTACGCT 3300	CURRENT APPLICATION NUMBER: US/09/765,555 CURRENT PILING DATE: 2002-05-24 PRIOR APPLICATION NUMBER: US 09/620,897 PRIOR APPLICATION NUMBER: US 60/177,468 PRIOR APPLICATION NUMBER: US 60/177,468 PRIOR FILING DATE: 2000-01-21 NUMBER OF SEQ ID NOS: 75 SOFTWARE: FASTSEQ for Windows Version 4.0 SOFTWARE: FASTSEQ for Windows Version 4.0 LENGTH: 3300 TYPE: DNA ORGANISM: Artificial Sequence FEATURE: ORGANISM: Partial sequence of pwal-ml and zinc finger OTHER INFORMATION: protein ZFPml	Query Match         97.2%;         Score 3207.2;         DB 10;         Length 3300;           Best Local Similarity         98.2%;         Pred. No. 0;         0.         0;         Gaps         0;           Matches 3242;         Conservative         0;         Mismatches         58;         Indels         0;         Gaps         0;           1 CCGACACCATCGAATGGGAAAACTTTCGCGGTATGGCATGATAGCGCCCGGAAGAG         0         CCGACACCATCGAATGGAAAACTTTCGCGGTATGGCATGATAGCGCCCGGAAGAG         0           1 CCGACACCATCGAATGTGAAAACTTTCGCGGTATATACGATGTCGCAGAGTATGCG         120         111111111111111111111111111111111111

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     CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA
                                            GCCTGCTGGGGGGAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
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                                                                                                                                      ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
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                                                                                                                                                                                                       pMal-m2
                                                                                                                                                                                                                                                      Score 3207.2;
Pred. No. 0;
0; Mismatches
TITLE OF INVENTION: expression in plants
FILE REFERENCE: 27801-20014.40
CURRENT APPLICATION NUMBER: US/09/765,555;
CURRENT FILING DATE: 2002-05-24
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 3300
                                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Partial sequence of
; OTHER INFORMATION: protein ZFPm2
US-09-765-555-15
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 98.2%;
Matches 3242; Conservative (
                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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1861 GAAGCGTATCCCCCAAACCAACCAACCCCCCAAACCCCCCCAAAACCCTCCCAAAACCCTCCCCAAAACCCTCCCCAAAACCCTCCCCCAAAACCCTCCCCCC	2881 CTGGTGCGCCATCAACGCACTCATACTGGCGAGAAGCCATACAAATGTCCAGAATGTGGC 2940

1381   CTGGCAAATATTCTGAAATGAGCTGTTCACAATTAATCATCGGCTCGTATAATGTGTGGA 1440	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAAGAT	1741 GCTCAATCTGGCTGTAGAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT 1800	1921   GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC   1980		2221 GCATGGTCAACATCGACAGCAAGTGATTATGGTGTAACGGTATGGCGACCTTC 2280 2281 AAGGGTCAACCATCCAAACCGTTGGCGTGACGGTAACGGTATGGCGCCCCGT 2340 2281 AAGGGTCAACCATCCAAACCGTTGGCGTGCTGAGCGCAGTATTAACGCCGCCAGT 2340 2281 AAGGGTCAACCATCCAAACGGTTGGCGTGCTGAGCGCAGTATTAACGCCGCCAGT 2340 2341 CCGAACAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA
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241 AACAACTGGCGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC 300 301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCCGATCAACTGGGTGCCAGC 360			ATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGGCGCAA   TGCGCGCCATTACCGACTCCGGGCTGGGCGTTGGTGCGGATACCTCGGTAGTGGGGATACC	GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGGGGTGAAGGGCAATCAGGGCCAGGCGGTGAAGGAAAACCACCTCGGGGCCCAATAAGGCAATCAGTGCTGCTGCTCGTCACTGGTGAAAAGAAAACCACCTGGCGCCCAATAAGGCAATCAGCTGCTCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACTGGCGCCTTTTAATGCAGCTGGCAGCTTTTAATGCAGCTTGCAGCGCTTTTAATGCAGCTGGCAGCGCTTTTAATGCAGCTGGCAGCTTTTAATGCAGCTGGCAGGCTTTTAATGCAGCTGGCAGGCTTTTAATGCAGCTGGCAGCGCGCGTTTTAATGCAGCTGGCAGGCTTTTAATGCAGCTGGCAGGGCTTTTAATGCAGCTGGCAGGGCTTTTTAATGCAGCTGGCAGGGCTTTTTAATGCAGCTGGCAGGCTTTTAATGCAGCTGGCAGGCTTTTAATGCAGCTGGCAGGGCTTTTTAATGCAGCTGGCAGCAGGCTTTTAATGCAGCTGGCAGCAGGCTTTTAATGCAGCTGGCAGCAGGCTTTTAATGCAGCTGGCAGCAGGCTTTTAATGCAGCTGGCACAGGCTTTTAATGCAGCTGGCACAGGCTTTTAATGCAGCTGGCACAGGCTTTTAATGCAGCTGGCACAGGCTTTTAATGCAGCTGGCACAGGCTTTTAATGCAGCTGGCACAGGCTTTTAATGCAGCTGGCACAGGCTTTTAATGCAGCTGGCACAGGCTTTTAATGCAGCTTGACAGGCTTTTAATGCAGCTTGACAGGCTTTTAATGCAGCTTGACAGGCTTTTAATGCAGCTTGACAGGCTTTTAATGCAGCTTGACAGGCTTTTAATGCAGCTTGACAGGCTTTTAATGCAGCTTGACAGGCTTTTAATGCAGCTTGACAGGCTTTAATTAA	1141 CCCGACTGGAAAGCGGCAGTGAGTGAATTAATGGTGACTCTTATG 1200  1141 CCCGACTGGAAAGCGGCAGTGAGCGCAATTAATGTGAGTTAGGTCACTCATTAG 1200  1201 GCACAATTCTCATGTTTGACAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA

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                                                                                                             CHER INFORMATION: Expression vector pMalc2cchbmp2
FEATURE:
COTHER INFORMATION: Expression vector pMalc2cchbmp2
FEATURE:
NAME/KEY: CDS
LOCATION: (1528)..(3453)
COTHER INFORMATION: /product = fusion protein MBP Cystatin C BMP-2
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2689)
COTHER INFORMATION: Faktor Xa Protease /position=388
COTHER INFORMATION: (Amino acid sequence)
COTHER INFORMATION: (Amino acid sequence)
LOCATION: (3067)..(3108)
COTHER INFORMATION: /spacer between Cystatin C andBMP-2
FEATURE:
NAME/KEY: misc_feature
LOCATION: (3067)..(3108)
COTHER INFORMATION: /spacer between Cystatin C andBMP-2
FUBLICATION INFORMATION:
AUTHORS: Zwick, M B.
TITLE: Expression vector pMal-X, complete sequence
JOURNAL: Anal. Biochem.
VOLUME: 264
SAGES: 87-97
DATE: 1998-11-01
DATE: 1998-11-01
DATE: 1998-11-01
DATE: 1998-11-01
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DATABASE ENTRY DATE: 2001-05-07
RELEVANT RESIDUES: 1528 - 3453
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82.0%; Score 2705.8;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2719; Conservative 0; Mismatches
                                                      LENGTH: 7373
TYPE: DNA
ORGANISM: Artificial Sequence
         SOFTWARE: Patentin Ver.
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Publication No. US20040087524A1
APPLICANT: Wiederanders, Bernd
APPLICANT: Waubach, Gunter
APPLICANT: Maubach, Gunter
FILE REFERENCE: 2945-101
CURRENT APPLICATION NUMBER: US/10/257,384A
FILE REFERENCE: 2045-101
CURRENT APPLICATION NUMBER: PCT/DE 01/01510
PRIOR APPLICATION NUMBER: DC 100-01-18
PRIOR PILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 19
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                              2461 TIGGCGAAAGATCCACGTATTGCCGCCACCATGBAAACGCCCAGAAAGGTGAAATCATG
                                                                                       CCGAACAICCCGCAGAIGICCGCTITCTGGIAIGCCGIGCGIACTGCGGTGAICAACGCC
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1611	2521 CCGAACATCCCGCAGATCTCCGCTTTCTGGTATGCCGTGCGTG
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SATE CACCATCAACACTATTATTTTTCCCCATCAACACCGACCCACCACCACCACCACCACCACCACCACCA	ATTGRAGGGGATAACAATTTCACACAGAAACAGCCGGTCGGTTTAGGTGTTTTCACGA   ATTGRAGGGGGATAACAATTTCACACAGGAAACAGCCGGTCGGTTTAGGTGTTTTCACGA   ATTGRAGGGGGATAACAATTTCACACAGGAAACGCCAGTCCGTTTAGGTGTTTTCACGA   GCACTTCACCACAAGGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATTCTGG   ATTAACGGCGATAAAGGCTATAAGGATTATGAAAATCGAAGAAGGTAAACAGGTAATCTGG   ATTAACGGCGATAAAGGCTATAACGGTTTAGAAATCGAAAGAAA

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                                                                                                     TGGTCGCATTGGGTCACCAGCAAATCGCGCGTTAGCGGGCCCCATTAAGTTCTGTCTCGG
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                                       RESULT 7

US-10-149-472-5

Sequence 5. Application US/10149472

Sequence 5. Application No. US20040029204A1

GENERAL INFORMATION:
APPLICANT: GOUBIN-GRAMATICA, FRANCOISE
APPLICANT: GOUBIN-GRAMATICA, FRANCOISE
APPLICANT: BLOCOMMUN, BERNARD
APPLICANT: PREVOST, GREGOIRE
TITLE OF INVENTION: METHOD FOR OBTAINING HUMAN CDC25 PHOSPHATASES AND METHOD
TITLE OF INVENTION: FOR IDENTIFYING HUMAN CDC25 PHOSPHATASE MODULATORS
TITLE OF INVENTION: MABER: US/10/149,472
CURRENT APPLICATION NUMBER: PR/10/10/2046

PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-14

PRIOR FILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 2000-09-21

NUMBER OF SEQ ID NOS: 14

SEQ ID NO S: 14

SEQ ID NO S: LENGTH: 8101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             // TYPE: DNA
// ORGANISM: Artificial Sequence
// FEATURE:
// OTHER INFORMATION: Description of Artificial Sequence: Synthetic
// OTHER INFORMATION: JM109 / DMAL - H8 Cdc25C strain
US-10-149-472-5
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2701 GGATCCTCCAGTCCCGGCAAGCCGCCGCGCCTGGTGGGAGG 2741
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US-10-343-859-8
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                                                                                                                                                     mutations
                                                             RESULT 8

US-10-343-659-8

US-10-343-659-8

Sequence 8, Application US/10343859

Publication No. US20040110161A1

GENERAL INFORMATION:
APPLICANT: Nanogen Recognomics GMBH

TITLE OF INVENTION: Method for detecting mute;
TITLE OF INVENTION: Method for detecting mute;
TITLE OF INVENTION: Mutoleotide sequences
FILE REFERENCE: 612,406-033

CURRENT APPLICATION NUMBER: US/10/343,859

CURRENT FILING DATE: 2001-07-13

PRIOR FILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 8

LENGTH: 6648
                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
 2709
              2701 GGATCCTCT
GGATCCTCT
2701
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                          ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT
                                                                CTGCAAGAACCGTACTTCACCTGGCGGCTGATTGCTGCTGCTGGGGGGTTATGCGTTCAAG
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CACCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC 600  TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 660	GCGCAA 8 GCGCAA 8 GCGCAA 8	Control   Cont	CGGTGA 10	AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAAAA	CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTAATGCAGCTGGCACGACAGGTTT 1140 CCCAAAAGCGGCCAGTGAGCCCAACGCAATTAATGCAGCTTAGCTCACTCA	CTGGCG 126	AATTCG 132        AATTCG 132	TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 1380	CIGGCAATAITCIGAAAIGAGCIGIIGACAAIIAATCAICGGCICGIAIAAIGIGIGGA 1440 	atigtgagcggataacaatttcacacaggaaacagccagtccgtttaggtgttttcacga 1500 	GCACTTCACCAACAAGGACCATAGAAAACTGAAGAAGGTAAACTGGTAATCTGG 1560 	AITAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT 1620 	-

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
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    DCATION: (1528)...(3189)
    OTHER INFORMATION: pMBP-c2X-ToxoP30dell1 (52-214aa)
    US-10-263-153-40

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81.5%; Score 2690.4;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches
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ORGANISM: Toxoplasma gondii
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Db   1741 GCTCAATCTGGCCTGTTGGAAATCACCCCGGACAAAGCGTTCCAGGACAAAGCTGTTAT   Qy	Oy 1861 Db 1861	Qy 1921 Db 1921	Qy 1981 Db 1981	Oy 2041 Db 2041	Oy 2101 G	0 Qy 2161 Db 2161	Qy 2221 Db 2221	0 Qy 2281 0 Db 2281	Qy 2341 0 Db 2341	Qy 2401 Db 2401	Qy 2461 Db 2461	Qy 2521 Db 2521	Qy 2581 Db 2581	OY 2641 AACAACAACAATAACAACAACAACACGGGATCGGGGATGGAGGAAGGA		10 ; GENERAL INCORPATION: ; APPLICANT: Abbott Laboratories ; APPLICANT: Maine, Gregory T.	
	721 GGGAAGGGGACTGGACTGGCCATGTCGGGTTTTCAACAAACCATGCAAATGCTGA 780 781 ATGAGGGCATCGTTCCCACTGCGATGCTGGCATGCCATGGGGGCGCGCA 840	TGCGCGCCATTACCGAGTCCGGGCTGCGGTTGGTGCGATATCTCGGTAGTGGGATACG	ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 9	961 GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 102	1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAGAAAAACCCCCCTGGCGCCCCAATA 1080 	114	1141   CCCGACTGGAAGCGGGGGGGGGGGGAATTAATGTGAGTTAGCTCACTCA	1201 GCACAATTCTCATGTTTGACAGCTTATCATGACTGCACGGGGGCCCAATGCTTCTGGCG 126 1201 GCACAATTCTCAACTTTGACAGCCTTATCATGACGGTGCACGACGACGACGACGACAATGCTTCTGGCG 126	TCAGGCAGCCATCGCAAGCTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 132	TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 	CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGG 	ATTGTCAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTT 	GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG	ATTAACGGCGATAAAGGCTATAACGGTCTCCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT 1 	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 1621 ACCGGAATTAAAGTCACCGTTGAGCATCGGATAAACTGGAAGAGAAATTCCCACAGGTT 1680	1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACGACGACGGCTTTGGTGGCTTA(174)	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGGCTGTAT 1800

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TITLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/263,153
CURRENT APPLICATION NUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PastSEQ for Windows Version 4.0
LENGTH: 7259
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                                                                                                                                                                                      81.5%; Score 2690.4;
99.8%; Pred. No. 0;
ative 0; Mismatches
                                                                                                  TYPE: DNA
ORGANISM: Toxoplasma gondii
                                                                                                                                                                                    Query Match
Best Local Similarity 99.8
Matches 2694; Conservative
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; SEQ 1D NO 35

: LENGTH: 7322

: TYPE: DNA

: ORGANISM: Toxoplasma gondii

: FEATURE:

: NAME/KEY: CDS

: LOCATION: (1528)...(3399)

: OTHER INFORMATION: pMBP-c2X-Toxop30del10 (52-284aa)

US-10-263-153-35
                                                                                                                             Score 2690.4;
Pred. No. 0;
0; Mismatches
                                                                                                                             Query Match
Best Local Similarity 99.8%;
Matches 2694; Conservative
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Publication No. US20040067239A1

GENERAL INFORMATION:

APPLICANT: Abbott Laboratories

APPLICANT: Maine, Gregory T.

APPLICANT: Ginsburg, Sanford R.

APPLICANT: Glisburg, Sanford R.

APPLICANT: Bliese, Timothy R.

TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF

FILE REPERENCE: 694-US-01

CURRENT APPLICATION NUMBER: US/10/263,153

CURRENT FILING DATE: 2002-10-22

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSEQ for Windows Version 4.0
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1991 CTGCAAGAACCGEACTCATTCACCTGGCCGCTGATTCCTGCTGACGAGGTTATCCGTTTCAAG   1991 CTGCAAGAACCGTACTCACCTGGCCGCTGATTGCTGCTGCTGGCGGCTTAAGCGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	RESULT 13 US-10-263-153-25 Sequence 25, Application US/10263153 Sequence 25, Application WS/10263153 Publication No. US20040067239A1 GENERAL INFORMATION: APPLICANT: Abbott Laboratories APPLICANT: Maine, Gregory T. APPLICANT: Ginsburg, Sanford R. APPLICANT: Bliese, IMPROVED ANTIGEN, ITILE OF INVENTION: IMPROVED ANTIGEN, ITILE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF FILE REFERRNCE: 6984-US.01 CURRENT APPLICATION NUMBER: US/10/263,153 NUMBER OF SEQ ID NOS: 74 SOFTWARE: FRAESEQ for Windows Version 4.0 SOFTWARE: FASTSEQ for Windows Version 4.0 SOFTWARE: TOXOPLASMA GOODII COGATION: (1528)(3429)
901 ACGATACCGAAGACAGCTCATGTTATATCCGGCCGTTAACCACCATCAAACAGGATTTTC 960 901 ACGATACCGAAGACAGCTCATGTTATATCCGGCCGTTAACCACCATCAACAGGATTTTC 960 901 ACGATACCGAACACAGCTCATGTTATATCCGGCCGTTAACCACCATCACACAGGATTTTC 960 901 GCCTGCTGGGGCAAACCAGCTGGAACACCTCTCAGGGCCAGCGGTGA 1020 902 GCCTGCTGGGGGCAAACCAGCTGGAACACCTCTCTCAGGGCCAGCGGTGA 1020 1021 AGGGCAATCAGCTGTTGCCCGGTTCACTGGTGAAAACACAGGTTCATTATTGCAGGCCAACAGTTT 1140 1031 AGGGCAATCAGCTGTTGCCCGGTTCACTGGAAAACACAGGTTT 1140 1041 GCCAAACCGCTCTCCCCGCGCGTTGACACATCATTAATGCACCTGCACACACA	1621   ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT   1680   1621   ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT   1680   1681   GCGGCAATTAAAGTCACCGCTTGAGCATCTCGGGACACACGACCGCTTTGGTGGCTAC   1740   1681   GCGGCAACTGGCGATGACTTTCTTCTGGCACACGACCGCTTTGGTGGCTAC   1740   1741   GCTCAATCTGGCGTTGAATCTTCTTCTGGGCACACGACCGCTTTGGTGGCTAC   1740   1741   GCTCAATCTGGCCTGAATCACCCGGACAAGCGTTCCAGGACAGCTGTAT   1800   1741   GCTCAATCTGGCCTGAAATCACCCGGACAAAGCGTTCCAGGACACGTGTAT   1800   1741   GCTCAATCTGGCTGATTGGCTGAAATCACCCGGACAAAGCGTTCACCGATCGCTGTT   1800   1801   GCGTTAACCTGGGATGCCTTACACGGACAAAGCGTTACCTGGGACAAGCTTACCTGGGACAAGCGTTACCTGGGACAAGCGTTACCTGGGACAAGCGTTACCTGGGACAAAGCGTTACCGGACAAAGCTTACCTGGGAAAACCTGGGAA   1920   1861   GAAGCGTTATCGCTGATTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA   1920   1861   GAAGCGTTATCGCTGATTATTAACAAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA   1920   1861   GAAGCGTTATCGCTGATTATTAACAAAAGATCTGCTGCCGAACCCGCCCAAAAACCTGGGAA   1920   1921   GAGATCCCGGCCTGGATTATAAAAAAAAAAAAACGAAAACCTGGCAAAAACCTGGGAA   1920   1921   GAGATCCCGGCCTGGATAAAAAACTGAAAAGCTACAAAAACCTGGCAAAAACCTGGCAAAACCTGGCAAAACCTGGCAAAACCTGGCAAAACCTGCAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGGCAAAAACCTGCAAAAAAAA

180 120 120 240 240 300 300 360 1020 1081 CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT 1140 360 420 420 480 480 540 540 600 9 9 9 9 9 720 720 780 780 840 840 900 900 960 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 301 ACGCGCCGTCGCAAATTGTCGCGCGATTAAATCTCGCGCCGATCAACTGGGTGCCGCG CGCGGGAAAAAGTGGAAAGCGGCGATGGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGC TGGTGGTGTCGATGGTAGAACGAAGGGGCGTCGAAGCCTGTAAAAGCGGCGGTGCACAATC TTCTCCCCCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG CGCGTCTGCGTCTGGCTGGCTGGCTGGCTTAAATATCTCACTCGCAATCAAATTCAGCCGATAG CGGAACGGGAAGGCGACTGGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA ATGAGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCAA TGCGCGCCATTACCGAGTCCGGGCTGCGCGTGCGGATATCTCGGTAGTGGGATACG 901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAGAAAAACAACCACCTGGCGCCCCAATA GCCTGCTGGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 961 GCCTGCTGGGGGGAAACCAGCGTGGATGCTGCAACTCTCTCAGGGCCAGGCGGTGA 

	CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGATGATGAAGGTCTG 2400	CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA	GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCCTAGCGCTGAAGTCTTACGAGAAGAG 2460	GAAGCGGTTAATAAAGACAAACCGCTGGCGGTGCGTGAAGTCTTACGAGGAAGAG 2460	TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520	TTGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAACGCCCAGAAAGGTGAAATCATG 2520	CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580	CGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580	GCCAGCGGTCGTCGACGGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640	GCCAGCGGTCGTCGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640	AACAACAACAACAATAACAATAACAATCAACCTCGGGATCGAGGGATTTCAGAATTC 2700	AACAACAACAACAATAACAATAACAACATCGGGGATGGGGGGGG	
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Search completed: August 3, 2005, 04:22:00 Job time: 1317.2 secs

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Sequence Sequence

Sequence Sequence

Sequence

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Run on:

Sequence:

Searched:

Database

Result

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compactible
OPPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,036
FILING DATE: 14-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                           US-08-891-848-2
US-08-125-462-5
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US-09-128-314-4
US-09-128-314-4
US-09-072-596-213
US-09-072-596-213
US-09-287-849-9
US-09-484-254
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US-09-418-314-3
US-09-630-940B-254
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US-09-630-940B-254
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US-09-630-940B-254
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Attwood, Michael R
APPLICANT: Hurst, David N
APPLICANT: Hurst, David N
APPLICANT: Way, Paul B
APPLICANT: Raynham, Tony M
APPLICANT: Raynham, Tony M
APPLICANT: Milson, Francis X
TITLE OF INVENTION: Amino Acid Derivatives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9623908.2
FILING DATE: 18-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 36822
REFERENCE/DOCKET NUMBER: 36822
REFERENCE/DOCKET NUMBER: RAN 4430/073
TELEPHONE: (973) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7475 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                               US-08-971-036-1; Sequence 1, Application US/08971036; Patent No. 5866884; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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COUNTRY: U.S.A.
ZIP: 07110
Nutley
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-640-882-2

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US-08-148-675A-2

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US-08-103-35

US-08-103-35

US-09-736-95-113-35

US-09-736-457-785

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                                                                                                                                                                                                 Length 7475;
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                                                                                                                                                                                                81.8%; Score 2700; 100.0%; Pred. No. 0;
REFERENCE/DOCKET NUMBER: RAN 4430/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 235-4387
TELEFAX: (973) 235-2363
INFORMATION FOR ESC ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7475 base pairs
                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                Query Match 81.8
Best Local Similarity 100.
Matches 2700; Conservative
                                                                                                                                                           ; HYPOTHETIC,
US-09-096-570-1
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                                                                                                                                                                                                                                                                                                                     TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG
                              TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
                                                                                   GCATGGTCCAACATCGACACCAGCAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
                                                                                                                                            AAGGGTCAACCATCCAAAACCGTTCGTTGGCGTGCTTGAGCGCAGCTATTAACGCCGCAGT
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                                                                                                                              AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT
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ZIP: 07110

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,570
FILING DATE:
PRIOR APPLICATION:
PRIOR APPLICATION WHEER: 08/971,036
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Attwood, Michael R
APPLICANT: Huret, David N
APPLICANT: Hones, Philip S
APPLICANT: Yones, Philip S
APPLICANT: Raynham, Tony M
APPLICANT: Wilson, Francis X
TITLE OF INVENTION: Amino Acid Derivatives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hoffmann-La Roche Inc
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09096570 Patent No. 6018020 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 38522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Nutley
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US-09-096-570-1
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1921 GAGNTCCCGGCGCTGGATAAAGAACTGAAAGGTAAAGGGCGCGCTGATGTTCAAC 1980		Db   2221   GCATGGTCCAACATCGACACCAGCAAATTATGGTGTAACGGTACTGCCGACCTTC   2280	GAAGCGGTTAATAAAGACAACGGCTGGGTGCGTGAGGCTGAAGGTCTTACGAGGAAGGCGTGAGGCTGAGGCTTAATAAAAGGCGCTGGGTGGCGTGGCGTGAGGCTTACGAGGAAGGGGTGGCGTAAGGCTGAAGTCTTACGAGGAAGAGGGTGGCGTAAGGCTGAAGTCTTACGAGGAGAGGGCTGAGGCGAAAGGCCGAAAAGGCCGAAAAGGCCCAAAAAGGCCCAAAAAGGCCAAAAAGGCCAAAAAGGCCAAAAAA	258 258 264 264	OY 2641 AACAACAACAACAATAACAACAACACCTCGGGATCGAGGGAAGGATTTCAGAATTC 2700	GENERAL INFORMATION:  GENERAL INFORMATION:  APPLICANT: Attwood, Michael R.  APPLICANT: Hurst, David N.  APPLICANT: Hurst, David N.  APPLICANT: Kay, Paul B.  APPLICANT: Rayhham, Tony M.  APPLICANT: Wilson, Francis X.  TITE OF INVENTION: Antiviral Medicaments	FILE REFERENCE: 20052 antiviral medicaments CURRENT APPLIACATION NUMBER: US/09/265,617B CURRENT FILING DATE: 1999-03-10 PRIOR PLILING DATE: 1999-03-30 PRIOR PLILING DATE: 1998-03-30 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver. 2.0
	AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAACCACCCTGGCGCCCCAATA		TGTCGCTCAAGGCGCACTCCGGTTGTGCAGGTCGTAAATCACTGCATAATTCG 132 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATTTTGCGCCGACATCATAACGGTT 138 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 138 CTGGCAAATATTCTGAAATGAGCTGTTGAAATAATCATCAGGCTCGTATAATCATGAATGA	ATTGTGGGGGATACAATTTCACAGGAAACAGCGGTCGTTTAGGTGTTTT   ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCGGTTTAGGTGTTTTT   ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTT   ATTGTGAGCGGAAACAACAATAGATTATGAAAACTGAAGAAAACTGGTAACTGAACTGAAC	TCGAGAAAGAT 1 TCGAGAAAGAT 1 TCCCACAGGTT 1 TCCCACAGGTT 1 TCCCACAGGTT 1	CTAC 174       CTAC 174 GTAT 180       GTAT 180	61

		1141 CCCGACTGGAAAGCGGCCAGTGAGCGCAACTAATGTGAGTTAGCTCACTCA	1261 TCAGGCAGCCATCGGAAGCTGTGGCTGTGCACGTCGTGCCAAAATCGTTGTGCGTCGTTGTGCGTCGTTGTGCGTCGTTGTGCGTCGT	1261 TCAGGCAGCCATCGGAAGCTGTGGTTGTGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1 1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGTT 1 1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAAAGGTT 1 1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 1	1381 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATGATGGCTCGTATAATGTGTGGG 1 	1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1 	1501 GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG 1 						1861 GAAGCGTTATCGCTGATTTATAACAACATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1 	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1	1981 CTGCAAGAACCGTACTTCACCTGGCGGTGATTGCTGACGGGGGTTATGCGTTCAAG 2
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LENGTH: 7475  TYPE: DNA  ORGANISM: Artificial Sequence FRATURE: OTHER INFORMATION: Description of Artificial Sequence: Vector and OTHER INFORMATION: Gene Fragments	Query Match         81.8%;         Score 2700;         DB 3;         Length 7475;           Best Local Similarity         100.0%;         Pred. No. 0;         0;           Matches 2700;         Conservative         0;         Mismatches         0;         Indels         0;           Qy         1 CCGACACCATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	GTCAATTCAGGGTGGTGAATGTGAAACCAGTAAGGTTATACGATGTCGCAGAGTATGCCG 	Oy         121 GTGTCTTTATCAGACCGTTTCCGCGTGGTGAACCAGGCCAGCCA	181 CGCGGGAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACGCGTGGCAC 241 AACAACTGGGGGGAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTGC [111111111111111111111111111111111111	DB 241 AACAACTGGCGGGCAAACAGTCGTTGCTGGTTGCCACCTCCCAGTCTGCCCTGC 300  Qy 301 ACGCGCCGTCGCAAATTGTCGCGGGCGATTAAATTCTCGCGCCGATCAACTGGGTGCCAGCG 360  Db 201 ACGCGCGTCGTCGTAAATTTTCTGCGGTGATTTAAATTCTCGCGCTCGATCAACTGGTGCAACG 360	361 TGGTGGTGTCGATGGTAGCGAGCGTCGAAGCCTGTAAAGCGGCGGTGCAATC 361 TGGTGGTGTCGATGGTAGAACGAAGCGGCGGTCGAAGCCTGTAAAGCGGCGGTGCAATC 361 TGGTGGTGGTGGTAACGAACGAACGAAGGTGGTGGTGGTGGTGAAGGAACGAAGGTGGTGGTGAACGAAGCGAGGTCGAAGCGAAGGTGGAAGGAA	421 TTCTCGGGAAGGGTCATCATTAACTATCGGTGATGACGAGGACGAGGTGCATGATCATTAACTATCGGTGATGATGACAAGGAACGAAGGAAG	481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGAGTTAATTTCTTGATGTCTCTGACCAGAGTTAATGTTCCTGGCGTTATTTCTTGATGTCTCTCGACCAGA	CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGGGGTGGAGCATC	Qy         601         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG         660           Db         601         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG         660	Oy 661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720	Qy       721       CGGAACGGGAAGGCGACTGGGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA       780         Db       721       CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA       780	OY 781 ATGAGGGCATCGTTCCCACTGCGATGCTGCTTGCCAACGATCAGATGGCGCTGGCGCAA 840 Db 781 ATGAGGGCATCGTTCCCACTGCGATGCTTGCCAACGATCAGATGGCGCTTGCCACGCAACATGCTTGCCAACGATGCTGCAACGATGCTGCAACGATGCTGCAACGATGCTGCCAACGATGCTGCAACGATGCTGCAACGATGCTGCAACGATGCTGCAACGATGCTGCAACGATCAACACGCGCAA 840	841 TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG	Db 841 TGCGCGCCATTACCGAGTCCGGGCTGCGGTTGGTGCGGATATCTCGGTAGTGGGATACG 900 Qy 901 ACGATACCGAAGGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGATTTTC 960

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1564 GACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGGT
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                                                                                                                                                                                                                                                                                                                                          DB 3; Length 5926;
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                                                                                                                                                                                                                                   TOPOLOGY: circular

MOLECULE TYPE: other nucleic acid

SESCRIPTION: /desc = "pEM delta R.adj to 1"

US-09-027-169-3
                                                                                                                                                                                                                                                                                                                                      Score 1417.6;
Pred. No. 0;
0; Mismatches
  NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/CDCKET NUMBER: 5789-3
TELECOMUNICATION INFORMATION:
TELEFAX: 919 813 3175
TELEFAX: 919 813 315
TELEFAX: 919 810 315
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGRH: 5256 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.6%;
Matches 1455; Conservative
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                                                                             2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
                                                                                                                                                         2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC
                                                                                                                                                                                                   TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
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                                                                                                                                                                                                                                                                                 GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
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| Patent No. 6420524
| GENERAL INFORMATION:
| TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
| TITLE OF INVENTION: ATP-DEPENDENT TRANSPOSITION PROTEINS
| NUMBER OF SEQUENCES: 15
| CORRESPONDENCE ADDRESS:
| STREET: 3605 Glenwood Ave.
| CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,169
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-09-027-169-3/c
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                                                                                                                                                                                                                 APPLICANT: UENO, EIICHI
APPLICANT: NOBUYUKI, FUJII
APPLICANT: OKADA, MASAHISA
TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR
TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2563 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 2622
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CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
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                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
ORIGINAL SOURCE:
ORGANISM: E. COLI
STRAIN: BL21 (DE3)
PUBLICATION INFORMATION:
AUTHORS: NOBUTUKI FUJII ET AL,
ITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: ERPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 5: PROM 1 TO 4557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,717
FILING DATE: 12-DEC-1996
CLASSIFFCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 35225/1995
FTLING DATE: 28-DEC-1995
ATTORNEY AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 28-18-18
REFERENCE/DOCKET NUMBER: 2084-031-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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100.0%; Pred. No. 0;
ative 0; Mismatches
                                                                                                                                RESULT 7
US-08-778-717-5
Sequence 5, Application US/08778717
Patent No. 6602689
GENERAL INFORMATION:
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TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 4557 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                Best Local Similarity 100.
Matches 1204; Conservative
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Best Local Similarity
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                 243 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC 302
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US-08-487-283A-18/c
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US-08-148-675A-2
IS-08-148-675A-2
| Sequence 2, Application US/08148675A
| Patent No. 5506121
| GENERAL INFORMATION:
| APPLICANT: Skerra, Arne; Schmidt, Thomas
| TITLE OF INVENTION: FUSION PEPTIDES WITH BINDING ACTIVITY FOR TITLE OF SEQUENCES: 2
| CORRESPONDENCE ADDRESS: | ADDRESSEE: Felfe & Lynch | STREET: 805 Third Avenue | STREET: New York City | STATE: New York City | CITY: New Yo
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Pred. No. 0;
0; Mismatches
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MEDIUM TYPE: Diskette, 5.25 inch, 360
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
COMPUTER: Diskette, 5.25 inch, 360
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,675A
FILING DATE: 3-NOV-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: DE 42 37 113.9
FILING DATE: 03-NOV-1992
ATTORNEY, AGENT INPORMATION:
NAME: TEAL, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: HUBR 1041
TELECHONE: (212) 888-3884
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH 13832 DASSES
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Best Local Similarity 99.8%;
Matches 1202; Conservative 0
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STRANDEDNESS: single
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PCT-US96-05611A-21/C
; Sequence 21, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Lenardo. Michael J.
; APPLICANT: Maris, Louis A.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Elleen Elliott
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APPLICANT: Matis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Rollins, Scott
APPLICANT: Rollins, Scott
APPLICANT: Squinto, Stephen P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Thomas, Thomas C.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
TITLE OF INVENTION: OF INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: 26
CORRESPONDENCE ADDRESS: 26
ADDRESSEE: Seth A. Fidel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.3%; Score 1199.2; DB 3; Length 5248; 99.8%; Pred. No. 0; ative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PET Trc SO5/NI
DESCRIPTION: prokaryotic expression vector
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.4Mb storage
COMPUTER: Macintocsh Cetris 610
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,208
FILING DATE: 02-MAY-1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
TELEFONE: (203) 776-1790
TELEFONE: (203) 776-1790
TELEFERM: (203) 776-1790
TELEFERM: (203) 776-1790
TELEFERM: (203) 776-176
SEQUENCE CHARACTERISTICS:
LENGTH: 5248 base pairs
TYPE: NUCLEAC ACID
STRANDEDNESS: DOUBLE
                                                                                                                                                                                STREET: Seth A. Fidel
STREET: 25 Science Park (Alexion)
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 99.8
Matches 1201; Conservative
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US-08-487-283A-18
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US-10-263-103-35/c
; Sequence 35, Application US/10263103
; Patent No. 681723
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PASTEUR
; APPLICANT: CHOVAILEY, Michel
; APPLICANT: El Habib, Raphaelle
; APPLICANT: Krell, Tino
; APPLICANT: Sodoyer, Regis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAC 3607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSE: Maurice M. Klee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: DET Trc SO5/NI
DESCRIPTION: prokaryotic expression vector
                                                                                                                                                                                                                                                                                                           ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
FILING DATE: 02-MAY-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.3%; Score 1199.2;
llarity 99.8%; Pred. No. 0;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION:

APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATORNEY/AGENT INFORMATION:
NAME: KIEW, MAUTICE M.
REFERENCE/DOCKET NUMBER: ALX-129
TELEFONNINICATION INFORMATION:
TELEFONNINICATION INFORMATION INFORMAT
                                                                                                                                                                                                           STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simil
Matches 1201; C
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                                       3782 TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGGATATCTCGGTAGTGGGATACG
                                                                                                                                                                                                                                               ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAACAGGATTTTC
                                                                                                                                                            GCCTGCTGGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
                                                                                                                                                                             GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
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                                                                                        ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ruppert, Siegfried J.W.
TITLE OF INVENTION: Construction of Full-Length cDNA Libraries
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,967
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.3%; Score 1199.2;
99.8%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08929967
Sequence 1, Application US/08929967
Sequence No. 5891637
GENERAL INFORMATION:
TITLE OF INVENTION: Construction of NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA May
CITY: South San Francisco
STRIE: California
COUNTRY: USA
ITP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb f
COMPUTER: HBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windberin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTONNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P103
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-2316
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 5443 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity 99.8
Matches 1201; Conservative
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                                                                                                                                                                                                                                              36.3%; Score 1199.2;
99.8%; Pred. No. 0;
ative 0; Mismatches
TITLE OF INVENTION: gp41 antigen
FILE REFERENCE: 01-1692-A
CURRENT APPLICATION NUMBER: US/10/263,103
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Petentin version 3.1
SEQ ID NO 35
LENGTH: 5312
                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: plasmid pET-cer
US-10-263-103-35
                                                                                                                                                                                                                                                                                Matches 1201; Conservative
                                                                                                                                       TYPE: DNA ORGANISM: Artificial
                                                                                                                                                                                                                                                                Similarity
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Best Local (
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Fatent No. 654010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Lodes, Michael A.
APPLICANT: Panger, Gary
APPLICANT: Panger, Gary
APPLICANT: Retter, Tom
APPLICANT: Retter, Marc
APPLICANT: Pan, Liqun
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR
ITILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT APPLICATION NUMBER: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: RestSEQ for Windows Version 3.0
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.8%;
Matches 1201; Conservative
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US-09-702-705-785
                                                                                                                                                                                                                    GCAC 3607
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US-09-702-705-785/c
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TYPE: DNA
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1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
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4198 ; CURRENT APPLICATION NUMBER: US/09/736,457 ; CURRENT FILING DATE: 2000-12-13 ; NUMBER OF SEQ ID NOS: 1864 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 785 600 ; DEGTH: 5502 600 ; TYPE: DNA 4078 US-09-736-457-785	660 Query Match 36.3%; Score 1199.2; DB 4; Length 5502; Best Local Similarity 99.8%; Pred. No. 0; Antches 1201; Conservative 0; Mismatches 3; Indels 0; Gaps 0	1   CCGACACCATCGAATGCTGCAAAACCTTTCGCGGTATGGTATGCGCCCGGAAGAGA 60	780 61 GTCAATTCAGGGTGGTGAAATGTGAAACCAGTAACGATGTCGCAGGTGTTGTCGCAGGTATGCCG 120	940  Qy 121 GTGTCTTATCAGACCGTTTCCCGCGTGGTGACCAGCCAGC	900  Qy 181 CGCGGGAAAAGTGGAAGCGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240	960  QY 241 AACAACTGGGGGGAAACAGTCGTTGCTGATTGGCGCCTCCAGTCTGGCCTTGC 300	1020  Qy 301 ACGCGCGTCGCAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTCGAGCG 360	1080  Qy 361 TGGTGGTGGTGGTAGAAGGGGGGTCGAAGCCTGTAAAGGGGGGGG	1140  Qy 421 TTCTGGGGAACGCGTCAGTGGGCTGATCATTAACTATCGGCTGGATGACCAGGATGCCA 480	1200 Qy 481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTTCTGACCAGA 540	Qy 541 CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGACTGGGCGTGGACATC 600	601 TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG [
Db   4257   TTCTCGCGCAACGCTCAGCTCATTAACTATCCGCTGGATGACCAGATGCCA   Oy   481   TTGCTGTGGAAGCTGCTGACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA	dy     601 TGGTCGCATTGGGTCACCAGCAATCGCGTGTTAGCGGGCCCATTAAGTTCTGTCTCGG       D	Oy 661 CGCGTCTGCGTCTGGCTGGCTGCCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG Db 4017 CGCGTCTGGCTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAT	Oy       721       CGGAACGGGAACGCGACTGGACTGCCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA         Db       3957       CGGAACGGGAACGCGACTGGAGTGCCCATGTCCGGTTTTCAACAAACCATGCAATGCTGA	Oy 781 ATGAGGGCATCGTTCCCACTGCGATGCTGCCAACGATCAGATGGCGCTGGGCGCAA Db 3897 ATGAGGGCATCGTTCCCACTGCGATGCTGGCAACGATCAGATGGCGCTGGGGCGCAA	OY 841 TGCGCCCCATTACCGAGTCCGGCTTGGTGCGGATATCTCGGTAGTGGGATACG	OY 901 ACGATACCGAAGACACTCATGTTATATCCCGCCGTTAACCACCATCAAACAGATTTTC	OY 961 GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGGGGTGA	OY 1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCCAATA	OY 1081 CGCAAACCGCCTCTCCCGGGGGTTGGCCGATTCATTAATGCAGGTTGGCACACGGGTTT DD 1597 CGCAAACCGCCTCTCCCCGGGGGTTGGCCGATTCATTAATGCAGCTGGCACACGGTTT	Oy       1141       CCCGACTGGAGGGCAGTGAGGGCAACGCAATTAATGTGAGGTTAGCTCACTCA	Oy 1201 GCAC 1204             Db 3477 GCAC 3474	SULT 1. Sequent Patent Patent APPLI

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                                                                                         GCCTGCTGGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
                                                                                                                              GCCTGCTGCTGCAACCAGCTGGCTCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
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US-09-614-124B-785/C
US-09-614-124B-785/C
Sequence 785, Application US/09614124B
Petent No. 6630574
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Enger, Gary
APPLICANT: Enger, Gary
APPLICANT: Retter, Darrick
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1199.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.8%;
Matches 1201; Conservative (
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US-09-614-124B-785
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Adh73599 Plasmid p
Adh73509 Plasmid p
Adh73601 Plasmid p
Adx23939 Nucleotid
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Ad18668 Plasmid p
Ad73089 MBP and z
Ad63622 MBP-human
Adc90431 Vector pl
Ad033532 Vector pG
Ad033532 Vector pG
Ad033531 Vector pG
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note= "CDS does not include start and stop codon"
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2740. 2790
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/bound moiety= "F1-f2 primer"
/*tag= c
/bound moiety= "F1-f1 primer"
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'bound moiety= "F2-b primer"
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|bound_moiety= "F2-f primer"
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3022. .3102
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Ab153238 Nucleotid
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Ad023613 DNA encod
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                  GenCore version 5.1.6
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                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) which is capable of specifically binding to a target uncleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target nucleotide sequence, where the expression of the target gene in the plant cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with Partial sequence of pWal-m3 and ZFPM3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the target gene.
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bound moiety= "F5-f primer"
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2401 GAMCCGSTTAMTANASCANCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	RESULT 2 AAD11592 ID AAD11592 standard; DNA; 3300 BP. XX AC AAD11592; XX DT 24-SEP-2001 (first entry) XX
1311   TGTGGCTCAAAGCGCGCACTCCCGTTCTGGATAATGTTTTTTGCCCCGCACATCAAACGTT   1380     1311   TGTGGCTCAAAGCGCACTCCCGTTCTGGATAATGTTTTTTGCCCCGCCCCCACATCAACGTT   1380     1312   TGTGGCAAATAATCTCAAAAACGCTTCTGCAATAATCTCTCGCCCCCTTCAACGTTTTTCACCGTTTTTTCACCGTTTTTCACCGTTTTTTCACCGTTTTTTCACCGTTTTTTCACCGTTTTTTCACCGTTTTTTCACCGTTTTTTCACCGTTTTTCACCGTTTTTTCACCGTTTTTTCACCGTTTTTTCACCGTTTTTCACCGTTTTTCACCGTTTTCACCGTTTTTCACCGTTTTCACCGTTTTCACCGTTTTCACCGTTTTCACCGTTTTCACCACTTTTCACCGTTTTCACCGTTTAAACGTTTTTCACCGTTTAAACGTTTTTCACCGTTTAAACGTTTTCACCACAAACGTTTCACCACAAACGTTTAAACGTTTTCACCACAAACGTTTAAACGTTTAAACGTTTAAACGTTTAAAACGTTTAAAACGTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAACACTTTAAAAACACTTTAAAACACTTTAAAACACTTTAAAAACACTTTAAAAACACTTTAAAAACACTTTAAAAACACTTTAAAAACACACAAAAACACTTTAAAAACACACAAAAACATTAAAAAA	2221 GCATGGTCCAACATCGACAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280

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                                               'transl except= (pos:3124 . .3126, aa:Ser)
'transl_except= (pos:3127 . .3129, aa:Ser)
'transl_except= (pos:3136 . .3138, aa:Val)
'note= "CDS does not include start and stop codon"
                                                                          /partial 2740. .2790 /*tag= b //bound moiety= "F1-f2 primer" 2770. .2850 /*tag= c
                                                                                                              *tag= c
bound_moiety= "F1-f1 primer"
824. .2889
                                                                                                                                                                                                      "F3-b2 primer"
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/bound_moiety= "F6-b2 primer"
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/bound_moiety= "F6-b1 primer"
3205. .3273
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bound_moiety= "F2-f primer"
916. _2973
                                                                                                                                                                                                                          "F4-f2 primer'
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867. 2940
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3119. .3192
/*tag= k
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                                        product= "ZFPAp3 protein"
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC
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                   Key
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) Which is capable of specifically binding to a target mucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target uncleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-Ap3 (APETALA3) and ZFPAp3 DNA
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1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60
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P-PSDB; AAE06000.
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                                        3001 CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCAGCACCAGTGGCTCCTTGGTTAGACAC 3060
                                                                         CAGCGTACCCACACGGTGAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGT 3120
                                                                                                                                          3121 GACTGCCGCGACCTTGCTCGCCATCAACGCACTCATACTGGCGAGAAGCCATACAAATGT 3180
                                                                                                                                                                 CAGCGCCCCCACCTGGAACGCCATCAACGCACTACTGGCGAGAAGCCATACAAATGT 3180
                                                                                                                                                                                                            CCAGAATGTGGCAAGTCTTTCTCCCAATCCAGCCATCTCGTCCGGCACCAAGGTACTCAC 3240
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          CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCAGCCAGAGCAGCTCCCTGGTGCGCCAC 3060
                                                                                                          CAGCGTACCCACACGGTGAAAACCGTATAAATGCCCCAGAGTGCGGAAATCTTTTAGC 3120
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.3207, aa:Gln)
.3210, aa:Ala)
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aa:Arg)
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bound moiety= "F1-f2 primer"
2770. 2850
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/bound_moiety= "F2-b primer"
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(pos:2872.
(pos:2875.
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(pos:3121.
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(pos:3205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Partial sequence of pMal-m1 and ZFPm1 DNA
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) Which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target within a target gene and allowing the ZFP binding to the target cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-m1 and ZFPm1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New zinc finger proteins, useful for modulating or regulating gene
expression and metabolic pathways in plants, e.g. for treating in the
plant cells a disorder that is associated with abnormal expression of the
target gene.
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                                                                                                                                                                                                                                                                                                         bound moiety= "F4-f2 primer"
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1076. 3141
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205. .3273
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*tag= e
/bound_moiety= "F2-f primer"
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119. 3192
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168. .3225
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Pred. No. 0;
0; Mismatches
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bound_moiety= "F3-b2
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC.
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21-JUL-2000; 2000US-00620897.
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Best Local Similarity 98.2%;
Matches 3242; Conservative (
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1081 CGCAAACCGCCTCTCCCCGCGCTTGGCCGATTCATTAATGCAGCTGGCACGACGGTTT 1140 1141 CCCGACTGGAAAGCGGCAGTGAGCGCAATTAATGCAGCTTGGCTCATTAG 1200	1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 1380 [1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTGCGCCGACATCATAACGGTT 1380 1381 CTGGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTGCGCTCGTATAATGTTGGGCTGGA 1440		GCACTTCACCAAGAACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG 	ATTAACGGCGATAAAGGCTATAACGGTCTGGCTGAAGTCGGTAAGAATTCGAGAAAGAT 162 	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 	1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTAC 1740 	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCGGACAAGCGTTCCAGGACAAGCTGTAT 1800 	ccgtttacctgggatgccgtacgttacaacggcaagctgattgcttaccgatgctgtt 186	1861 GAAGCGTTATCGCTGGTTTATAACAAAGATCTGCTGCCGAACCCGCCAAAACCTGGGAA 1920 	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGACGCGCTGATGTTCAAC 1980 	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040 	2041 TATGAAAACGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100 	2101 GGTCTGACCTTCCTGGTTGACTTAAAAACAAACACATGAATGCAGACACCGATTAC 2160 	2161 TCCATGGCGGAGGCGCTTTAATAAAGGGAAACAGGGATGACCATCAACGGCCGGTGG 2220 
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	AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGCTGCTTGCAACTGGCCTTGCTTG	ACGCGCCGTCGCAATTGTCGCCGCGATTAAATCTCGCGCCCGATCAACTGCGGTGCC 	TGGTGGTGTCGATGGTAGAACGGGTGTCGAAGCCTGTAAAGCGGGGGTGCA TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGA 	TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGA 	CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGA 	TGGTCGCATTGGGTCACCAGCAAATCGCGGTGTTAGCGGGCCCATTAAGTTCTGT 	CGCGTCTCGCGTCTGGCTGGCATAAATATCTCACCTCGCAATCAAATTCAGCCC	CGGAACGGGAAGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACGATGCAAAT 	ATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGG 	TGCGCGCCATTACCGAGTCCGGGCTGCGCGTGCGGATATCTCGGTAGTGGGATACG 	ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAACAGGATTTTC 	GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGC 	AGGGCAATCAGCTGTTGCCCGTCTCGTGAAAGAAAACCACCTGGGGCCCAATA	CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACCACA
ATGGTGCAAAACCTTTCC GGTGAATGTGAAACCAGT GGTGAATGTGAAACCAGT GGCGTTTCCCGCGTGGT GACCGTTCCCGCGTGGT GAAGCCGTTCCGGGGGGGGGG	CAAACAGTCGTTGCTGAI 	AATTGTCGCGGCGATTAA 	GGTGGAACGAGGGGGGG GGTCAGTGGGCTGATCAT 	TGCCTGCACTAATGTTCC                  TGCCTGCACTAATGTTCC	TATTATTTCTCCCATGP	TCACCAGCAAATCGCGCT	GGCTGGCTGGCATAAATP	CGACTGGAGTGCCATGTC	TCCCACTGCGATGCTGGT                 TCCCACTGCGATGCTGGT	CGAGTCCGGGCTGCGCGT	CAGCTCATGTTATATCCC	AACCAGCGTGGACCGCTT	GTTGCCCGTCTCACTGGT	TCCCCGCGCGTTGGCCG
CGA GGT GGT GGT AGT AGT	8-8			A – 66	ACAG	766 1665	5=5	AAGG	TCGI   TCGI	rtac       rtac	A — A	5 — 5 9 — 5	£=5	Ę==
1 CCGACACCAI 61 GTCAATTCAG 61 GTCAATTCAG 121 GTGTCTCTTA 121 GTGTCTCTTA 121 GTGTCTCTTA 121 GTGTCTCTTA 121 GTGTCGTAAA	241 AACAACTGGCG( 	301 ACGCGCCGTCG 301 ACGCGCCGTCG 361 TGGTGGTGTCG	421 TTCTCGCGCA 	481 TTGCTGTGGA           481 TTGCTGTGGA	541 CACCCATCA         541 CACCCATCA				781 ATGAGGGCA          781 ATGAGGGCA	841 TGCGCGCCA:          841 TGCGCGCA'			1021 AGGGCAATCA           1021 AGGGCAATCA	1081 CGCAAACCGC

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metabolic pathway regulator;
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note= "CDS does not include start and stop codon"
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bound_molety= "F6-b1 primer"
1205. .3273
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/bound_moiety= "F6-b2 primer"
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2770. .2850
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168. 3225
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modulation; plant technology; agriculture;
                                                                                                      Partial sequence of pMal-m2 and ZFPm2 DNA
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC
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2719. .3270
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3119. .3192
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740. .2790
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GCATGGTCCAACATCGACAGCAAGAAATTATGGTGTAACGGTACTGCCGACCTTC
                GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
                                                                   AAGGCTCAACCATCCCAAACCGTTCGTTGGCGTGCTCAAGCGCAGCTATTAACGCCGCCAGT
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc flinger protein (ETP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target nucleotide sequence, where the expression of the target gene in the plant cells is modulating or regulating agene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-m2 and ZFPm2 DNA New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of target gene. 4; Page 140-142; 156pp; English WPI; 2001-465325/50. P-PSDB; AAE06002. Example 

ö DB 4; Length 3300; Sequence 3300 BP; 847 A; 874 C; 876 G; 703 T; 0 U; 0 Other; 58; Indels Score 3207.2; Pred. No. 0; 0; Mismatches Query Match 97.2%; Best Local Similarity 98.2%; Matches 3242; Conservative C

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the
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1261 1321 1321 1321 1381 1441 1441 1501	1561 ATTAACGGGGATAAAGGCTATAACGGTCGCTGAAGTCGGTAAGAAATTCGAGAAAGT 1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGT 1571 ACCGGAATTAAAGTCACCGTTGAGCATCCGCTGAAGAAATTCGAGAAAGTT 1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1681 GCGGCAACTGACGATCACCTGAATAACTGGAAGAAATTCCCACAGGTT 1681 GCGGCAACTGACGATGACATTATCTTCTGGGCACCACGACCACGACCACGCTAC 1741 GCTCAATCTGGCCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1741 GCTCAATCTGGCCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1741 GCTCAATCTGGCCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1761 GCTCAATCTGGCCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1771 GCTCAATCTGGCCTGAAATCACCCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1771 GCTCAATCTGGCCTGAAATCACCCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1771 GCTCAATCTGGCCTGAAATCACCCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1771 GCTCAATCTGGCCTGAAATCACCCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1771 GCTCAATCTGGCCTGAAATCACCCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1771 GCTCAATCTGGCTGAAATCACCCCCGGACAAAGCGTTCCAGGACAAGCTGTAT		2221 GCATGGTCCAACATCGACAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280  2221 GCATGGTCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280  2281 AAGGGTCAACCATCCAAACGGTTGGTGGTGCTGAGCGCAGTATTAACGCCGCCAGT 2340  2281 AAGGGTCAACCATCCAAACGGTTGGTTGGTGTGTGTGTATTAACGCCGCCAGT 2340  2281 AAGGGTCAACCATCCAAACGGTTGGTTGGTGTGTGTGTTAAACGCCGCCAGT 2340  2341 CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTTGCTGGTGATGAAGGTCTG 2400
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2640 2580 GCGCCACCATGGAAAACGCCCAGAAAAGGTGAAATCATG 2520 2580 2640 2700 2700 2760 AGCGATCCTGGCCACCACCACCACCACCCAC 2820 2880 2880 2940 2940 AGCCTGGTGCGCCACCAACGTACTCACACGGGGGAGAAG 3000 3060 3120 3180 3180 3240 AAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTAGC 3120 AGGCCGGCCAGTACCCGTACGACGTTCCGGACTACGCT 3300 COGCTGGGTGCCGTAGCGCTGAAGTCTTACCAGGAAGAG GCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC GATGAAGCCTCAAAAACGCGCAAATTCGAGCTCG TGCCCAGAGTGCGGCAAATCTTTTAGCACCAGCGGCTCC PATACTOGCGAGAGAGCOTACAAATGTCCAGAATGTGGC SGTAAGTCCTTCAGCCAGAGCAGCTCCCTGGTGCGCCAC AACCGTATAAATGCCCAGAGTGCGGCAAATCTTTAGT ZATCAACGCACTCATACTGGCGAGAGCCATACAAATGT ATCAACGCACTCATACTGGCGAGAAGCCATACAAATGT cccaarccagccarcregreegecaccaacgracreac 

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                                                        TIGCTGTGGGAAGCTGCCTGCACTAATGTTCCCGGCGTTATTTCTTGATGTCTCTGACCAGA
                                                                                                                             CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC
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                                                                                                                                                                                                                                                                                                                                                                                       New fusion protein of maltose-binding protein and Cdc phosphatase, useful for identifying phosphatase modulators for regulating the cell cycle.
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maltose binding protein; MBP; Cdc25C phosphatase;
); Cdc25B3; cyclin-dependent kinase; CDK; cell division;
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                                                                                                                                                                                                            14-DEC-1999; 99FR-00015722.
30-MAY-2000; 2000FR-00006883.
21-SEP-2000; 2000FR-00012008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.9%;
Matches 2707; Conservative 0
                                                                                                                                                                           13-DEC-2000; 2000WO-FR003496
                                                                                                                                                                                                                                                                                                                     Goubin-Gramatica F,
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                    Cdc25B2;
                                                                       Homo sapiens.
                                                                                                                                          21-JUN-2001
 Fusion pro
Cdc25B1; (
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Cdc25C phosphatase, amine; Cdc25 phosphatase; spontaneous alopecia; alopecia; proliferative disease; parasitic disease; viral infection; neurodegenerative disease; myopathy; anglogenesis; psoriasis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cdc25 phosphatase. The specification describes the use of arylasubstituted secondary or tertiary amines for the production of medicaments for inhibiting Cdc25 phosphatases, sepecially Cdc25 phosphatases. The amines of the invention are used for treating spontaneous alopecia or alopecia induced by exogenous products or spontaneous alopecia or alopecia induced by exogenous products or radiation. They are also used for treating tumoural or non-tumoural proliferative diseases, parasitic diseases, viral infections, neurodegenerative diseases or myopathy. Examples of non-tumoural proliferative diseases are e.g. angiogenesis, psoriasis or restenosis. The amines are also useful for inhibiting the proliferation of microorganisms (especially yeasts) and in the treatment of all disorders conventionally treated with vitamin K or its derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cdc25 Phosphatase inhibiting medicaments, useful e.g. for treating tumor diseases, viral infections, neurodegenerative disease or alopecia, containing new or known aryl-substituted amines.
                                                 2641 AACAACAACAATAACAATAAAAAAAAAAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence represents pMAL-H8Cdc25C, a plasmid encoding
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                                                                 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAATTCGAGAAAGAT
                                                                                                    1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT
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Query Best Match	Query Match 82.0%; Score 2705.8; DB 6; Length 8101; Best Local Similarity 99.9%; Pred. No. 0; Matches 2707; Conservative 0; Mismatches 2; Indels 0; Gans 0;	Db	
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ර සි	GTCAATTCAGGGTGGTGAATGTGAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG	දු අ	1141 CCCGACTGGAAAGCGGCAGTGAGCGCAATTAATGTGAGTTAGCTCACTCA
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<u>ک</u> ۾	CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACGCGTGGCACGCGTGGCAACGCGGGAAAAGTGGAAAGGGGGGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC	S G	TCAGGCAGCCATCGGAAGCTGTGGTATGCTGTGCAGGTCGTAAATCACTGCATAATTCG 
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<u>۾</u> ج	361 TGGTGGTGTCGATGGAAGCGGGCGTCGAAGCCTGTAAAGCGGGGGGGG	& 8 8	ATTGTGAGCGGATAACAATTTCACACAGGAACAGCCGGTCGTTTAGGTGTTTTCACGA 
p ó	TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCAGATGACAACGCGTGAACGAAC	ري و و	gcacticaccaacaagaccatagattatgaaactgaagaagtaaactggtaatctgg 1 
à a	481 TIGCIGIGGAAGCTGCCTGCACTAAIGTTCCGGCGTTATTTCTTGAIGTCTCTGACCAGA 540	è 4	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTGCGGTAAGAATTCGAGAAAGAT 1620 
\$ <b>9</b>	CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGGCGTGGAGCATC	oy Pp Oy	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT 1680 
S QS	TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCCGGGCCCATTAAGTTCTG 	දු සු	1681 GCGGCAACTGGCGCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTAC 1740 
oy Db	CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG	b oy	1741 GCTCAATCTGGCCTGTTGGCTGAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT 1800 
දු පි	CGGAACGGGAAGCGACTGGAGTGCCATGTCCGGTTTTCAACAACCATGCAATGCTGA 	& 8 &	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 
ે જે ક	ATGAGGGCATCGTTCCCACTGCGATGCTGCCAACGATCAGATGCCGCTGGGCGCAAACGATCAGATGCCGCTGGGCGCAAAAAAAA	b &	1861 GAAGCGTTATCGCTGATTATAACAAAGATCTGCTGCGAACCCGCCAAAAACCTGGGAA 1920 
3 & 8	TGCGCGCCATTACCGAGTCCGGGCTTGCGTTGGTGGTGGTATTCTCGGTAGTGGGGGTACGTTGGCGCGATATCTCGGTAGTGGGGGTACGTTGGCGCGATATCTCGGTAGTGGGGGTACGTTGGCGCATATCTCGGTAGTGGGATACGTTGGCGCGTTGGTGGCGGTTACTCGGTAGTGGTAATTCTCGGTAGTGGATATCTCGGTAGTGGATATCTCGGTAGTGGATATCTCGGTAGTGGATATCTCGGTAGTAGTATACTGGTAATACTG	ري و م	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGGCGCGCTGATGTTCAAC 1980 
े हें	ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC	e o	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040
8 8 8	GCTGCTGGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGGAACCTGCTGCTGCAACTCTCTCAGGGCCAGGCGGGGAACGCTGCTGCAACTCTCTCT	& 8 8	2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100 
ò	AGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAAAAA	ò	2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAACACATGAATGCAGACACCGATTAC 2160

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GGTCTGACCTTCCTGGTTGACCTGATTAAAACAAACACATGAATGCAGACACCGGATTAC 2160
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               TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
                        2161 TCCATCGCAGAGGTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
                                              GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
                                                                             AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT
                                                                                       GCCAGCGGTCGTCAGACTGTCGATGAAGCCCCTGAAAGACGCGCAGACTAATTCGAGCTCG
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                                                                                                              P30 antigen, Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                       encoding MBP-ToxoP30del8(82-294aa) fusion protein.
                      ВЪ.
                  AD023608 standard; DNA; 7259
                                                                                                                                                                                                                                              02-OCT-2002; 2002US-00263153
                                                                                                                                                                                                                                                                     02-OCT-2002; 2002US-00263153
                                                                  (first entry)
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PATEL C B.
GINSBURG S R
BLIESE T R.
                                                                                                                                                             Toxoplasma gondii
Synthetic.
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(PATE/) (GINS/) (BLIE/)

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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30de12C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30de13C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence of Toxo30de13C(52-30aa) MBP-Toxo30de14C(52-294aa) and MBP-Toxo30mIX1 funsion proteins. (I) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120
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                                                                                                                      Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
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Ginsburg SR,
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Matches 2694; Conservative
Patel CB,
                                                   WPI; 2004-304563/28
                                                                        P-PSDB; ADO23609
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                                                        P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, Toxo30del2C, Toxo930 MIXI, useful for detecting presence of IgM or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7322 BP; 1887 A; 1844 C; 1934 G; 1657 T; 0 U; 0 Other;
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                           DNA encoding MBP-ToxoP30dell0(52-284aa) fusion protein.
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81.5%; Score 2690.4; DB 12;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 6; In
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                                                                                                                                                                                                                                                                                                                                                                     Bliese
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                                                                                                                                                                                                                            02-OCT-2002; 2002US-00263153
                                                                                                                                                                                                                                                         02-OCT-2002; 2002US-00263153
(first entry)
                                                                                                                                                                                                                                                                                      (MAIN/) MAINE G T.
(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
                                                                                                                                                                                                                                                                                                                                                                  Maine GT, Patel CB,
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P-PSDB; ADO23614.
                                                                                                                   Toxoplasma gondii.
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                                                                                                                                                                                                                              TTCTCGCGCAACGCGTCAGTGGGCTCATTAACTATCCGCTGGATGACCAGGATGCCA
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                                                                                                                                                                                                                                                                                                                                                                               CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC
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	UULT 10 )23603 ADO23603 standard; DNA; 7352 BP. ADO23603; 01-JUL-2004 (first entry)	DE DNA encoding MBP-ToxoP30de14C(52-294aa) fusion protein.  XX  KW  NX  KW  P30 antigen, Toxo30de13C; Toxo30de12C; ToxoP30 MIX1;  KW  Toxoplasma gondii; ds; gene.  XX  CS  Toxoplasma gondii.  SS  Synthetic.  XX  NX  NX  NX  NX  NX  NX  NX  NX  N		Note purified polypeptide having sequence identity to amino acid generate of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, PT sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.  Example 2; Fig 19; 114pp; English.  XX  XX  Example 2; Fig 19; 114pp; English.  CC Toxo30del3C, Toxo30del2C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del3C; Toxo30del3C and ToxoP30 MIX1 sequence of Toxo30del3C p30 antigen sequence of Toxo30del3C p30 antigen sequence in which at least one of the five C-terminal cysteine amino acid sequence in which alanine, or comprising the amino acid sequence is substituted with alanine, or comprising the amino acid sequence of Som MBP-Toxo30del4C(52-294aa) and MBP-Toxo30del4C(52-2
	ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT	1741 GCTCAATCTGGCCTGTTGGCTCAAATCACCCGGACAAGCGTTCCAGGACAAGCTGTAT 1800	1921 GAGATCCCGGCGCTGGATAAGAACTGAAAGCGAAAGGCGCGCTGATGTTCAAC 1980	2101 GGTCTGACCTTCTGGTTGACCTGATTANAACACACATGAATGCAGACACCGATTAC 2160 2161 TCCATCGCAGAAGCTGACCTTTAATAAAGGCGAAACACACATGAATGCAGACACCGATTAC 2160 2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220 2221 GCATGGTCCAACATCGACACACAGCAAACTGAATTATGGTGTAAACGGTACTGCCGACCTTC 2280 2221 GCATGGTCCAACATCGACACACAGAAAGTGAATTATGGTGTAAACGGTACTACCGACCTTC 2280 2281 AAGGGTCAACCATCCAACACGTTCGTTGGCGTGAGTGTAAACGGTACTAACGCACCAGT 2340 2281 AAGGGTCAACCATCCAAACGTTCGTTGGCGTGCTGAGCGCAGTATTAACGCCCCAGT 2340 2281 AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGTATTAACGCCCCAGT 2340 2381 AAGGGTCAAACAGTTCGTTGGCGTGCTGAGAGCTTAACGCCCCAGT 2340 2381 CCGAACAAAAGAGTTCCTCGAAAACTTTTGCTGATGATGAAGAGTCTG 2400 2341 CCGAACAAAAGAGTTCCTCGAAAACTTTTGCTGATGATGAAGAGTCTG 2400 2401 GAAGCGGTTAATAAAAAGACTTCCTCGAAAACTTCTGCTGATGATGAAGGTCTG 2400 2401 GAAGCGGTTAATAAAAAGACTTCCTCGAAAACTACTGCTGATGATGAAGAGATCTG 2400 2401 GAAGCGGTTAATAAAAAGACTATCTCCGAAAACTATCTGCTGAACTATGATGAAGAAGAGTCTG 2400 2401 GAAGCGGTTAATAAAAAACCTGTGGTGACTGATGAAGAGATCTTACGAGGAAAGG 2460

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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30del3C. Toxo30del2C and ToxO930 MIXI sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30del3C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence closen from MBP-Toxo30del3C(52-300aa), MBP-Toxo30del4C(55-294aa) and MBP-Toxo30MIXI fusion proteins. (I) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of [IN]/IgM antibody complexes. The presence sequence represents DNA encoding a MBP-TOXO930 fusion protein of the invention.
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                                                                                                                                  Novel purified polypeptide having sequence identity to amino acid sequence of F93 antigen of Toxoplasma gondii e.g. Toxo30de13C, Toxo30de12C, Toxo930 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                        Bliese TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
81.5%; Score 2690.4;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches
                                        Ginsburg SR,
                                                                                                                                                                                                                                      Example 2; Fig 15; 114pp; English
                                      Patel CB,
                                                                           2004-304563/28
BLIESE T R.
                                                                                               P-PSDB; AD023599
                                        Maine GT,
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC 600 TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 660 TGGTTGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGCCCATTAAGTTCTGTCTCGG 660	CGCGTCTGCGTCTGGCTGGCTGAAAATATCTCGCTGTGAAATTCAGCCGATAG 720	CGGAACGGGAAGCCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA 780 	ATGAGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA 840 	TGCGCCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG 900	ACGATACCGAAGACACCTCATGTTATATCCCGCCGTTAACCACCATCAACAGGATTTTC 960	GCGGTGA 10         GCGGTGA 10	AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAACCACCCTGGCGCCCAATA 1080	114	CCCGACTGGAAAGCGGGCGGTGAGCGCAATTAATGTGAGTTAGCTCACTCA	126	TAATTCG 132	AACGGTT 1	CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATGATCGGCTCGTATAATGTGTGGA 1440 		VATCTGG 15	AAAGAT 162         aaagat 162	ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT 1680 

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                                                                                                     P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel purified polypeptide having sequence identity to amino acid acquence of F30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or antibodies to Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 12; Length 7370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7370 BP; 1900 A; 1856 C; 1950 G; 1664 T; 0 U; 0 Other;
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99.8%; Pred. No. 0;
iive 0; Mismatches
                                                                      DNA encoding MBP-ToxoP30MIX1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ginsburg SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 31; 114pp; English
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                                     01-JUL-2004 (first entry)
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Matches 2694; Conservative
                                                                                                                                                                                                                                                                                                                                                                             MAINE G T.
PATEL C B.
GINSBURG S R.
BLIESE T R.
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Synthetic.
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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-Toxo30del3C(52-300aa), MBP-Toxo30del4C(52-294aa) and MBP-TOXO30MIX1 fusion proteins. (I) is useful for detecting the presence of IgM
                                           2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
                        GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
                                                                                            GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG
                                                                                                                                                                                                         or IgG
                                                                                                                                  CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or antibodies to Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ТŖ,
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding MBP-ToxoP30MIX5 fusion protein.
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(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
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                                                                                                                                                                                                                                                                                                                                               standard;
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 antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.
                                                                                                                                                                                                              ACGCCCCCCAAATTGTCCCCCGCATTAAATCTCCCCCCATCAACTGGCTCCACCC
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                                                                                                                             CCGACATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCGGAAGAGA
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Pred. No. 0;
0; Mismatches
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                                                                BP; 1900 A; 1857
                                                                                    81.5%;
99.8%;
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Best Local Similarity 99.8
Matches 2694; Conservative
                                                               Sequence 7370
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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30del3C and ToxoP30 MXX1 sequences, having 1-6 amino acid sequence to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30del3C P30 antigen sequence is substituted with alamine, or comprising the amino acid sequence chosen from MBP-Toxo30del3C(52-30de) MBP-Toxo30del3C(52-294aa) and MBP-Toxo30MIX1 fusion proteins. (I) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-Toxo930 fusion protein of the invention.
                                                                                                                                                                                       Novel purified polypeptide having sequence identity to amino acid sequence of F930 antigen of Toxoplasma gondii e.g. Toxo30de13C, Toxo30de12C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7370 BP; 1900 A; 1857 C; 1950 G; 1663 T; 0 U; 0 Other;
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                                                                                        Ginsburg SR,
                                                                                                                                                                                                                                                                                           Example 5, Fig 33; 114pp; English.
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Matches 2694; Conservative
                                                                                        Patel CB,
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                                                                                                                      GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC 2160
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
                                                                                                                               P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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                                                                                                 DNA encoding MBP-ToxoP30del2(52-311aa) fusion protein.
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                                                                       01-JUL-2004 (first entry)
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Best Local Similarity 99.8
Matches 2694; Conservative
                                                                                                                                                                                                                                                                                                                                             (MAIN/) MAINE G T.
(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
                                                                                                                                                                                                                                                                                                                                                                                                                   Maine GT, Patel CB,
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P-PSDB; ADO23595.
                standard;
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1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGCAGAATCACTGCATAATTCG   1320   1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGCAGAACTCTGCATAATTCG   1320   1321 TGTCGCTCAAGGCGCCTCCGGTTGGGTATGGTTTTTTGCGCCGACACTCATAACTGTT   1380   1321 TGTCGCTCAAGGCGCACTCCTGGATAATGTTTTTTTGCGCCGACATCATAACGGTT   1380   1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTTGCGCCGCACTCATAACGGTT   1380   1381 CTGGCAAATATTCTGAAATGACTTGACAATTAATCATCGCCGCCACTCATAATGTGTGGA   140   1411 ATTGTGAGCGGATAACAGTTGACAATTAATCATCGCCTCTAAGGTGTTTTCACGA   1500   1411 ATTGTGAGCGGATAACAATTAACAAATGACCAGTAAACAGCCAGTTTAGGTGTTTTCACGA   1500   1501 GCACTTCACCAACAAGAGCAAAAAGCAAAAAGAAAAAAAA	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680		ccgrtthcctgggatgccgfacgtfacaacggcaagctgattgctfacccgatcgctgrt gaagcgrtatcgctgatttataacaaagatctgctgccgaacccgccaaaaacctgggaa 	921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGGCGCGCTGATGTTCAAC 	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCGGGGTTATCGGTTCAG 2040  1981 CTGCAAGAACCGTACTTCACCTGGCTGTT[	DI GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC 	161 TCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCGTGG 	2221 GCATGGTCCAACATCGACACGCAAGTGATTATGGTGTAAGGGTACTGCCGACCTTC 2280 	2281 AAGGGTCAACCATCCAAACCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT 2340 [11]
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/organism="synthetic construct"
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Methods and compositions to modulate expression in plants
Patent: WO 0152620-A 16 26-JUL-2001;
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AUTHORS Barbas, C.F., Stege, J.T., Guan, X. and Dalmia, B.  TITLE Methods and compositions to modulate expression in plants JOURNAL Patent: WO 0152620-A 18 26-JUL-2001; The Scripps Research Institute (US); SYNGENTA AGRICULTURAL DISCOVERY, INC. (CA) Location/Qualifiers 1. 3300   organism="synthetic construct"   /mol type="unassigned DNA"   /mol type="unassigned DNA"   /mol type="unassigned DNA"   /mol type="unassigned"   /mol type="unassigned"	ORIGIN  Query Match  Best Local Similarity 98.4%; Pred. No. 0;  Matches 3248; Conservative 0; Mismatches 52; Indels 0; Gaps 0;	Qy         1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60	Db   61 GTCAATTCAGGGTGGTGAATGTGAAACGTTATACGTTATACGATGTCGCAGAGTATGCCG 120	181 CGCGGGAAAAGTCGAAGCGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACCGCGTGGCACGCGTGGCACGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGAGGCGAGGCGAGGCAGAAAAGCGGCG	Qy 241 AACAACTGGGGGAAACAGTGGTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC 300 241 AACAACTGGGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTGC 300	Qy         301 ACGCGCCGTCGCAAATTGTCGCGCGAATTAAATCTCGCGCCGATCAACTGGGGTGCCAGCG         360           Db         301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG         360	Qy         361 TGGTGGTGTCGATGGTGGAACGAACGGCGTCGAAGCCTGTAAAGCGGGGGTGCACAATC 420           Db         361 TGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGGGTGCACAATC 420	421 TICTCGCCCAACGCGTCAGTGAGTCATTAACTATCCGCTGGATGACCAGGATGCCAGATGACTATCAGTGGCTGAACGGTGGGATGACTAGCTGGGTTGGCTGGATGACCAGGATGCCA	Qy         481         TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACAGA         540           Db         481         TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTCTTGATGTCTCTGACAGA         540	541 CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC 541 CACCCATCAACAGTATTATTTTTCTCCCATGAAGACGGTACGGGACTGGGGGGGG	601 IGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 	Qy 661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720	Qy         721         CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA         780           Dh         721         CGCAACGGAAGGCGAACGAGTGCCATGCTCCATGTCCGATGCTGA         780	781 ATGAGGGGATCGTTCCCACTGCGATGCTTGCCACGATCAGATGGCGCTGGGCGCAA
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/note="Plasmid pMAL-c2x"	Query Match 81.8%; Score 2701; DB 6; Length 6648; Best Local Similarity 99.8%; Pred. No. 0; Matches 2704; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	Oy 1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60	Qy         61 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG         120           Db         61 GTCAATTCAGGGTGGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG         120	Oy 121 GTGTCTTATCAGACCGTTTCCCGCGTGGAACCAGGCCAGCCA	Qy         181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240           Db         181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240	Oy 241 AACAACTGGGGGGCAAACAGTGGTGGTGATTGGGGTTGCCACTCCAGTCTGGCCCTGC 300	Qy         301 ACGCGCTCGCAAATTCTCGCGGCGATTAAATCTCGCGCCGATCAACGGTGCCAGCG         360           10 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG         360	QY         361 TGGTGGTGTCGATGGTAGAACGAGGGGGTCGAAGCCTGTAAAGCGGGGGTGCACAATC 420           Db         361 TGGTGGTGTCGATGGTAGAAGCGGGGGTCGAAGCGGGGGGGG	Qy         421 TTCTCGGCCAACGCGTCAGTGATCATTAACTATCGCTGGATGACGATGCCA 480           Db         421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCGGTGGATGACAGGATGCCA 480	Oy 481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGGGTTATTTCTTGATGTCTCTGACCAGA 540	Qy         541 CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGGACTGGGCGTGGAGCATC         600           bb         541 CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGGGCGTGGGCGTGGAGCATC         600	Oy 601 TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 660	Qy         661 CGCGTCTGCGTCTGGCTGGCTTAATATCTCACTCGCAATCAAATTCAGCCGATAG 720           Db         661 CGCGTCTGCGTCTGGCTGGCTGGCTTAATATCTCACTCGCAATCAAT	Oy 781 ATGAGGGCATCGTTCCCACTGCGATGCTGGCCACCATCAGATGGCGCTGGGCGCAA 840			901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAACAGGATTTTC	Oy 961 GCCTGCTGGGGCAAACCAGCGTGGACGGCTTGCTGCAACTCTCTCAGGCCAGGCGGTGA 1020
	Qy         2041         TATGAAAACGCCAAGTACGACATTAAAGACGTGGGGGGGG	OY 2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAACATGAATGCAGACACCGATTAC 2160 	Qy         2161         TCCATCGCAGAGGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG         2220           Db         2161         TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAACAGCGATGACCATCAACGGCCGTGG         2220	QY       2221       GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC       2280         Db       2221       GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC       2280	Qy 2281 AAGGTCAACCATCCAAACCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCGGT 2340	Oy 2341 CCGAACAAAGAGTTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA	QY 2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG 2460	OY 2461 TIGGGGAAAGATCCACGTATTGCCGCCACCATGGAAACGCCCAGAAAGGTGAAATCATG 2520	Qy     2521     CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGC     2580       Db     2521     CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGC     2580	Oy 2581 GCCAGCGGTCGTCACACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640	Qy         2641 AACAACAACAATAACAATAACAACAACCTCGGGATCGAGGGAAGGATTCAGAATTC         2700           Db         2641 AACAACAACAATAACAACAACAACCTCGGGATCGAGGGAAGGATTCAGAATTC         2700	Qy         2701 GGATCCTCT 2709           Db         2701 GGATCCTCT 2709	RESULT 8 AX377531 LOCUS AX377531 6648 bp DNA linear PAT 18-MAR-2002 DEFINITION Sequence 8 from Patent WO0212553. ACCESSION AX377531 VERSION AX377531.1 GI:19573717	ALYMOUS Synthetic construct ORGANISM synthetic construct ORGANISM synthetic construct other sequences; artificial sequences.	RS Kappel, A., Polakowski, T., Pignot, M., Windhab, N., Behr Muth, J.	JILLE MECHON LOT ACCECTING MUCATIONS IN MULEOCIAE SEQUENCES JOURNAL PAtent: WO 021253-A B 14-FEB-2002; Nanogen Recognomics GmbH (DE) FEATURES Location/Qualifiers	rce 1	/mol_type="unassigned DNA" /db_xref="taxon:32630"

QY         2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACAAA	2281 AAGGGTCAACCATCCAAACCGTTGGGGGGGGGGGGGGGG	Db   2401	Oy 2581 GCCAGCGTCGTCAGACTGTCGAAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640  Db 2581 GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640  Oy 2641 AACAACAACAACAATAACAACAACAACCTCGGGATCGAGGGAAGGATTCAGAATTC 2700  Db 2641 AACAACAACAACAATAACAACAACAACCTCGGGATCGAGGGAAGGATTTCAGAATTC 2700  Oy 2701 GGATCCTC 2709  Db 2701 GGATCCTCT 2709		AUTHORS ALTWOOD, M. R. and Hurst, D. N. TITLE ANTIVIRAL PEPTIDE DERIVATIVES JOURNAL PATENT: WO 9822496-A 1 28-MAY-1998; HOFFMANN LA ROCHE (CH) SOUTCE LOCATION/Qualifiers 1 . 7475 Mol_type="unidentified" /Mol_type="unidentified" /db_xref="taxon:32644"	Query Match 81.8%; Score 2700; DB 6; Length 7475; Best Local Similarity 100.0%; Pred. No. 0; Matches 2700; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy I CCGACACCATGGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60
GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA	CCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA	1321 TGTCGCTCAAGGCGCTTCTGGATAATGTTTTGCGGCAAATGATGTT 1380  1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTGCGCCGACATCAAAACGTT 1380  1381 CTGGCAAATATTCTGAAATGACTTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440  1381 CTGGCAAATATTCTGAAATGACTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440  1411 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCGTTTAGGTGTTTCACGA 1500  1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCGTTTAAGTGTTTTCACGA 1500	GCACTTCACCAACAAGGACCATAGATATGAAAACTGAAGGAGAAACTGGAATTCAGG 1	1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTAC 1740	GAAGCGTTATGGCTGATTTATAACAAGATCTGCTGCGGAACCGGCGAAAACCTGGGAA	1981 CTGCAAGAACGGTACTTCACCTGGCCGCTGATTGCTGACGGGGTTATGCGTCAAG 2040 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGCGTGG

181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGTTACATTCCCAACCGCGTGGCAC 240 241 AACAACTGGCGGCAACACGTCGTTGCTGATTGCGGTTGCCACCTCCGATCTGGCCCTGC 300 241 AACAACTGGCGGCGAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC 300 301 ACGCGCGTGGCAAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360 301 ACGCGCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360 301 ACGCGCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360 301 ACGCGCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360 301 TGCTGGTGGTTAAATTGTCGCGGCGATTAAATCTCGCGCGATCAACTGGGTGCCACATC 420 421 TTCTCGCGCAACGCGTCAGTGGCGTCATTAAATTATCTTCGCTGGATGCCA 480 481 TTGCTGGTGGATCGATGGTCATTAACTATACTATTCTTGATGTTCTTGACGATGCCA 480 481 TTGCTGGTGGATCGATGGGCGTGATCATTAACTATTCTTGATGTTCTCTGACCAGA 540 481 TTGCTGGTGGAACGCGCTCAATGTTCCGGCGTTAATTTCTTGATGTTCTCTGACCAGA 540 481 TTGCTGTGGAAGCGACTCATAATTTTCTTCGTCGTGGAGCATC 600 691 TTGCTGTGGAAGCGACTCATAATTTTCTTCGTCTTGACCAGA 540 601 TTGCTGTGGAACGCACTAATGTTCCCCATGAACGCTTGGACCAGA CCAGA CCAGA CCACCAACAACACGTAACAACACGTTAAATTTTCTTCGACCAGACCAGA CCACCAACAACACAAC	
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1501 GCACTTCACCAACAACCATAGATTATGAAACTGAAGAAGGTAAACTGGTAATCTGG 1560 	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGT 1620 1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAATTCGAGAAAGT 1620	1621 ACCGGAATTAAAGTCACCGTTCAGCATCCGGATAAACTGGAAGAAATTCCCACAGGGT 1680	1681 GCGGCAA         1681 GCGGCAA	1741	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGCTAAGAGGCGCGCTGATGTTCAAC 1980	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040	2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100	2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAACAAACACATGAATGCAGACACCGATTAC 2160 2101 GGTCTGACCTTCCTGGTTGATTAAAAACAAACAAACAAAC	2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220	2221 GCATGG        2221 GCATGG	2281	2341 CCGAACAAAGAGTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA	2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG 2460 	2461 TTGGGGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520 	2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580
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421 TTCTCGCGCAACGCGTCAGTGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 480 	3TTATTTCTTGATGTCTCTGACCAGA 54	CACCCATCAACAGTATTATTTTCTCCCATGAACACGGTACGCGACTGGGGCGTGGAGCATCCATC	GCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 	AGCCGATAG	1000   1000	ATGAGGCATCGTTCCCACTGCGATGGTGGTTGCCAACGATCAGATGGCGTGGGCGCAA 8	STGGGATACG	ACGATACCGAAGACAGCTCATGTTATATCCGCCGTTAACCACATCAACAGGATTTTC 9	GGTGA 1 GHHH GGTGA 1	APAACCACCTGGCGCCCAATA 108	CCTCTCCCCGGGGGGGGGGTTCATTAATGCAGTGGGACGACGACAGGTTT	CCCGACTGGAAAGCGGCAGTGACGCAATTAATGTGAGTTAGCTCATTAG 120	ATGCTTCTGGCG	AATCACTGCATAATTCG	TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 138	CTGGCAATATTTCTGAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGGA 14	ATTGTGAGCGGATAACAATTTCACACAGGAACAGCCGGTCCGTTTAGGTGTTTTCACGA 150 ATTGTGAGCGGATAACAATTTCACACAGGAACAGCCCGGTCCGTTTAGGTGTTTTCACGA 150

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90 Ag	3 4 5 4 5 7	8 6 8 6 8 6 8	o a o a o	4	6666	6	8 8 6 8 6
		Other sequences; artificial sequences.  REFERENCE 1  AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrensdorf,H. and Muth,J.  TITLE Method for detecting mutations in nucleotide sequences JOURNAL Patent: WO 0212553-A 9 14-FEB-2002;  Nanogen Recognomics GmbH (DE)  FEATURES 1.: 9191  Accation/Qualifiers 1: 9191  Accation/Qualifiers 2: 9191  Accamism="synthetic construct"  Anol type="unassigned DNA"  Ab xref="taxon:32630"  Anote="pwALc2x-mutS Plasmid"	y Match Local S hes 2701	Qy         61 GTCAATTCAGGGTGGTGAAACGTGAAACGTTATACGATGTCGCAGGTATGCCG         120           Db         61 GTCAATTCAGGGTGGTGAAACGTAAACGTTATACGATGTCGCAGAGTATGCCG         120           Qy         121 GTGTCTTATCAGACGTTTCCCGGGTGGTGAACCAGGCCAGCCA	Qy         181 CGCGGGAAAAAGTGGAAGCGGGATGGCGGAGCTGAATTACATTCCCAACCGGTGGCAC 240           Db         181 CGCGGAAAAAAGTGGAAGCGGGATGGCGGAGCTGAATTACATTCCCAACCGGTGGCAC 240           Qy         241 AACAACTGGCGGCGAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTGC 300           Db         241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGC 300	Qy         301 ACGCGCCGTCGCAAATTGTCGCGCGATTAAATCTTCGCGCCGATCAACTGCGTGCCAGCG         360           HIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	421 TTCTCGCGCAACGCGTCAGTGGCTGATCATTAACTATCGCTGGATGACCAGGATGCCAGGATGCCAGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGATGCTGCAGGATGACCAGGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCTGCGCGTGAGTGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCCAGATGCTGCCAGATGCTGCCAGATGCTATTTCTTGATGTCCCTGACCAGATGCTAGATGTTCCTGATGTTCCTGATGTCCCAGATGCAGATGCTAGATGTTCCTGATGTCTCTGATGTCTCTGATGTTCTTGATGTCTCTGATGTCTCTGAGATGCTCCAGAGATCCAGATGCTCCCAGATGCAGATCCAGAATTTTTTTT

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and Heinrikson, R.L.
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                      GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC
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100   ACCORTACCGAGGAGCTCATGTTGTTGTGTGTGTGTGTATTCCGGTAGTGGGATACC 900	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGT 1620

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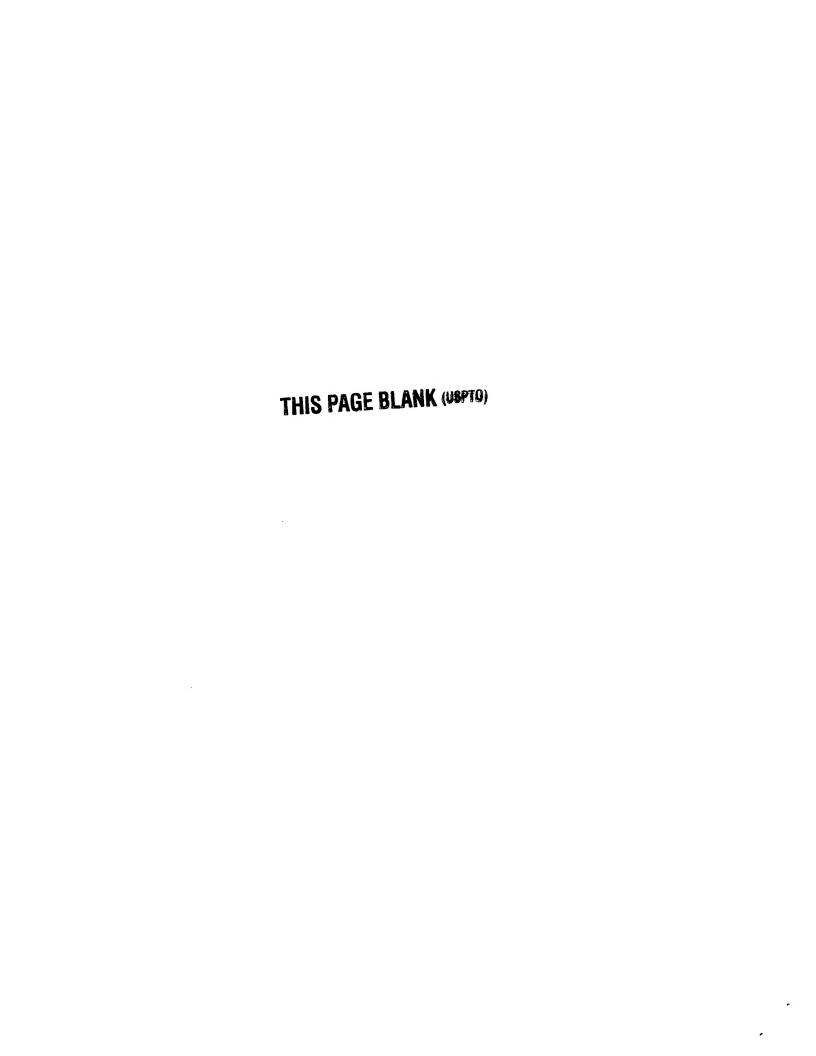
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                                  Length 6706;
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                                  DB 12;
                                                                                 0; Mismatches
                                  Score 2631;
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/ product = "lac "aab86558.1"
/ brotein id="aab86558.1"
/ brotein id="aab86558.1"
/ brotein id="aab86558.1"
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EDSSCYIPPLTTIKQDFRLLGGTSVDRLLQUSQGAVKGNQLLPVSLVKRKTTLAPNT
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LIKNKHMNADTDYSIAEAARNKGETAMTINGPWAWSNIDTSKVNYGYTVLPTFKGGPS
KPFVGVLSAGINAASPNKELAKEFLERYTLLTPBGLEANWKDKPLGAYALKSYEBELAK
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NNNNNNNNIGIEGRISEFGSSRVDLQASLALAVVLGRRDWENPGYTGLNRLAAHPPF
ASWRNSEARTDRPSQQLRSLNGEWQLGCFGG"
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DKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLFNPPKTWEEIPALDKEL
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IBLDLNSGKLIBSFRPEERSPWMSTFKVLLCGAVLSRVDAGGEQLGRRIHYSQNDLVB
SVYTEKHLTDGWTVRELCSAAITWSDNTAANLLTTIGGFREITAFHNWGHYTRL
DRWEPELNEAIPNGGBYTKWPYAMATTIRKLITGELTLASRQCIDWWEAVVAGEL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKFSRIVVIYTGSQATWDERNRQIA
'note="derived from commercially available vector pMal-p2
(New England Biolabs)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="maitose binding protein-lacz alpha peptide
fusion protein precursor"
/protein_id="AAB86559.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="malE-lacza fusion"
/product="maltose binding protein-lacz alpha peptide
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1478. ,4338
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                                                                                                                                                                                                                        note="transcriptional repressor"
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/standard_name="M13 origin (+ -)"
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protein_id="AAB86560.1"
db_xref="G1:2623824"
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1528. 2976
/gene="malE-lacZa fusion"
/note="MBP-lacZa, MBP modified
secretion signal sequence"
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1528. .2976
/gene="malE-lacZa fusion"
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/codon_start=1
/transl_table=11
                                                                                               'note="E. coli gene"
                                                                                                                                                                                                                                                                             table=11
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'gene="lacI"
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/gene="bla"
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K0994C10-DKFZp566O B0156F05-

DKFZp434J

HH06A02y B0124F04 -DKFZp434D

DKFZp566K DKFZp434D

В0137Н04-

DKFZĎ566C hggađa2H1

DKFZp566G

B0192A07-

Perfect score:

Sequence:

OM nucleic -

Run on:

Scoring table:

Searched:

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Database

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Colletotrichum trifolii

Colletotrichum trifolii

Colletotrichum trifolii

Eukaryota: Rungi; Ascomycota; Pezizomycotina; Sordariomycetes;

Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;

mitosporic Phyllachoraceae; Colletotrichum.

Sa Samac.D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,

Cheung,F. and Fraser.C.M.

ESTS from mycelia of Colletotrichum trifolii race 1

AL Unpublished (2002)

Other ESTS: ESTG3248

Contact: Deborah A. Samac

Department of Plant Pathology

University of Minnesota

495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

Tel: 612 625 1243

Fax: 651 649 5058 at Minnesota

TiGR sequence name: MTSAH67TV More information is available at:

www.medicago.org

Seq primer: (gtA AtA CgA CtC Act AtA ggg C).

Location/Qualifiers

ir. 794

// Ab yref="Hryon-arce" in the colletotrichum trifolii"
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/clone=mpgSCTB-67"
/tissue_type="mycelia"
/dev_stage="Young, actively growing mycelia (3 days after incellation) grown in liquid culture (cutin minimal medium containing 2%gluocee)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="DSCT"
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 2sp2 ; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtll from
Strategene and packaged using disgapack packaging extracts.
An aliquot of the amplified library was used to transduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ751936 10ear EST 18-JUL-20 EST632499 DSCT Colletotrichum trifolii cDNA clone pDSCT8-67, mRNA
                                                                                                                                                               CA886082
AL044407
AL039076
AL038025
CK394397
CK394397
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AL039589
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CA887583
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AL038811 I
CA890032 I
CB862099 I
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CB862524
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CR886082
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BQ751936.1 GI:21907341
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Copyright (c) 1993 - 2005 Compugen Ltd.
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E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DHSalpha which were plated onto medium with X-gal for selection of recombinants."
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                                                                                         23.6%; Score 778; DB 5; Length 79
98.7%; Pred. No. 4.9e-219;
ive 0; Mismatches 10; Indels
                                                                                                 Local Similarity 98.7
nes 784; Conservative
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CK394523 779 bp mRNA linear EST 30-DEC-2003 hggada4D08 Gland Cell Amplified cDNA Library Heterodera glycines

Heterodera glycines

Heterodera glycines

Heterodera glycines

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Bukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;

Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.

I (bases 1 to 779)

S Wang,X., Allen,R., Gao,B., Goellner,M., Maier,T., Baum,T.,

Hussey,R. and Davis,E.

Submission: Wang, Allen, Gao, Goellner, Maier, Baum, Hussey, Davis

Unpublished (2003)

Conteat: Tom Maier

Department of Plant Pathology, Baum Lab

Iowa State University

351 Bessey Hall, Ames, IA 50011, USA ö 146 999 266 326 540 386 480 266 cDNA Library, single pass 446 420 506 360 300 CATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATC 240 CCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTTTATCAGACCGTTTCCCGC 719 GTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAAACGCGGGAAAAAAGTGGAAGCGGCGATG GCGGAGCTGAATTACATTCCCAACCGCGTGGCACCAACTGGCGGGCAAACAACTTG CTGATTGGCGTTGCCACCCCCGGCCCTGCACGCGCCGCCGAAATTGTCGCGGC CCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACGTTTCNCCGC GTGGTGAACCAGGCCAGCCATTTCTGCGAAAACGCGGGAAAAAGTGGAAGCGGCGATG GCGGAGCTGAATTACATTCCCAACCGCGTGGCACAACAACAGCGGGCAAACAGTCGTTG CTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCGCCGTCGCAAATTGTCGCGGCG GGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTG 327 ATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGGTGGTGGTGGTAGAACGAAGC GTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTCTCC 359 GITCCGGCGITAITICITGAIGICICIGACCAGACACCCATCAACAGIAITAITITCICC CATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATC Gaps ö 779; Length Indels Score 770.6; DB 7; Pred. No. 7.6e-217; 0; Mismatches 5; Amplified Email: trmaier@iastate.edu Heterodera glycines Gland Cell Location/Qualifiers CK394523.1 GI:40389794 EST. Query Match
Best Local Similarity 99.4%;
Matches 773; Conservative C Tel: 515-294-8854 Fax: 515-294-9420 567 299 ò 셤

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BQ751655 T93 bp mRNA linear EST 18-JUL-2002 EST612218 DSCT Colletotrichum trifolii cDNA clone pDSCT6-59, mRNA sequence.
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Colletotrichum trifolii
Colletotrichum trifolii
Colletotrichum trifolii
Colletotrichum trifolii
Sukaryote, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.

1 (bases 1 to 793)
Samac, D. A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,
Cheung, F. and Fraser, C.M.
ESTS from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
                                                                                                                                     1045 CACTGGTGAAAAGAAAACCACCCTGGCGCCCAATACGCAAACCGCCTCTCCCGGGGGT
                                                                                                                                                                                                                        121 ATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTTTCT
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                                                            GCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGC
                                                                                                                    AIGTICCGGCGTIAITICTIGAIGICICIGGCCAGACACCCAICAACAGIAITITICI
                                                                                                                                                                                                                                                                            CCCATGAAGACGGTACGCGACTGGGCCATCTGGTCGCATTGGGTCACCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATGTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGA
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                                                                                                                                                                                                                                                                                                                                                                        218n06_pl AtMl Arabidopsis thaliana cDNA clone MPMGp2011N06218
5-PRIME, mRNA sequence.
CK118014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; tosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis. (bases 1 to 769)
Feilner, T., Immink, R.G.H., Cahill, D.J. and Kersten, B. Generation of a cDNA expression library from Arabidopsis inflorescence meristem
                                                                           GCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCGTCTGGCTTGGCTTGGCTT 686
                                     ccecretraecececcarraacrrererecececererecerereceresera 180
                                                                                                                                                            ATGTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATG 806
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="inflorescence meristem"
/dew stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSE111"
/clone_lib="AtM1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Institute 73 , D-14195 Berlin, Germany
Tel: +49(0)30/84131648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/mol_tope="columbia"
/db_xref="GABI:956015"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: +49(0)30/84131128
Email: Kersten@molgen.mpg.de
Insert Length: 769 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plate: 218 row: N column: 6
Seq primer: pQE65.
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CK118014
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Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="mycelia"
/dev stage="Young, actively growing mycelia (3 days after incollation) grown in liquid culture (cutin minimal medium containing 2%ducose)."
/lab_host="DHSalpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  806 bp mRNA linear EST 18-JUL-2002 DSCT Colletotrichum trifolii cDNA clone pDSCT3-64, mRNA
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/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 28p2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtll from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
                                                                                                                                                                                                                                                                                                                                                                                                         Colletotrichum trifolii
Colletotrichum trifolii
Colletotrichum trifolii
Eukaryotea, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetes incertae sedis, Phyllachorales, Phyllachoraceae,
mitosporic Phyllachoraceae, Colletotrichum.
I (bases I to 806)
Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,
Cheung, F. and Fraser, C.M.
ESTS from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
Other_ESTS: EST631782
                                                                                                        CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTG
                                                                                                                                         CCCATCAACAGTATTATTTTCTCCCATGAACACGGTACGCGACTGGGCGTGCAGCATCTG
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                GCTGTGGAAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA
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TIGR sequence name: MTSAC64TV More information is available at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www.medicago.org
Seq primer: (gtA AtA CgA CtC ACt AtA ggg C).
Location/Qualifiers
Location/Qualifiers
i. 806
/organism="Colletotrichum trifolii"
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/strain="race 1"
/db_xref="taxon:5466"
/clone="pDSCT3-64"
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                                                                                  /tissue_type="mycella"
/dev stage="Young, actively growing mycella (3 days after inoculation) grown in liquid culture (cutin minimal medium containing 2%quose)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEORI; isolate: 292, cDNA was prepared from polyAtenriched RNA The cDNA was prepared from polyAtenriched RNA The cDNA was ligated into Lambda gtll from Stratagene and packaged using dispapeck packaging extracts. An aliquot of the amplified library was used to transduce E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after ECORI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DHSalpha which recombinants."
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/note="Vector: pBluescript SK+; Site_1: BcoRI; Site_
/note="Vector: pBluescript SK+; Site_1: BcoRI; Site_
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23.1%; Score 762; DB 5; Length 793;
Best Local Similarity 99.1%; Pred. No. 2.8e-214;
Matches 777; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                   organism="Colletotrichum trifolii"
                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:5466"
/clone="pDSCT6-59"
                     Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/strain="race 1"
    Other ESTs: EST632217
                                                                                                                                                                                                                                                                             . 793
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lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DHSalpha which were plated onto medium with X-gal for selection of recombinants."
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                                                                                                                           GACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGT
                                                                             22.9%; Score 755.4; DB 5; llarity 97.4%; Pred. No. 2.5e-212; Conservative 0; Mismatches 16;
                                                                                          Similarity
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                                                                                                          481 GCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA
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                                                                        GCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA
                                                                                                                                                CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTG
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CB863541 689 bp mRNA linear EST 22-APR-2003 HH04A08y HH Hordeum vulgare cDNA clone HH04A08 3-PRIME, mRNA sequence.

RESULT 6 CB863541/c LOCUS DEFINITION

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                                                 Hordeum vulgare
Hordeum vulgare
Hordeum vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 689)
Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCCGCGTGGTGAACCAGGCCAGCCACTTTCTGCGAAAACGCGGGAAAAAGTGGAAGGGGGGTGTTTCTGCGAAAAACGGGGAAAAAGTGGAAAGCGTGCTGCGTGGTGAAAACGCGGGGAAAAAGTGGAAAGCG
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                                                                                                                                                                                                                                          Contact: Stein Nils
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Email: stein@ipk-gatersleben.de
Insert Length: 689 Std Brror: 0.00
Plate: 4 row: A column: 8
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99.6%; Pred. No. 2.3e-191;
live 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              day

    .689
    /organism="Hordeum vulgare"
/mol_type="mRNA"
    /cultivar="Sloop"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="GABI:555198"
/db_xref="taxon:4513"
/clone="HH04A08"
/tissue_type="coleoptile"
/dev_stage="coleoptile, 1 di
/lab_host="DH108"
                                                                                                                                                                                    Graner, A.
Barley ESTs from coleoptile tissue
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                 GI:30058100
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Viruses; environmental samples.

(bases; environmental samples.

Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Mead, D., Azam, F. and Rohwer, F.

Genomic analysis of uncultured marine viral communities
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
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AY080106 Scripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3GGL, genomic survey
                                                                  AACCAGGCCAGGTTTCTGCGAAAACGCGGG-AAAAAGTGGAAAGCGGATGGCGGA
                                                                                                                                                                                                                                                                                                                                                 331 AATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGTCGATGGTAGAACGAAGCGCC
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San Diego State University
S500 Campanile Dr. San Diego, CA 92102,
Tel: 6195941316
Pax: 619595676
Email: forest@sunstroke.sdsu.edu
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DKPZp566E0346_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
AL038548
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This is the 5' sequence of the clone insert
Clone from 8. Wiemann, Molecular Genome Analysis, German Cancer
Clone from 8. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DRFZ); Email 8 wiemann@dkFz heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No 81 sequence
available.
This clone (DKFZD566E0346) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
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Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                      TTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAG
                                                                                                                                                                                                                                                                                                                 33 GGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAAACCAGTA
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Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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ilarity 99.6%; Pred. No. 7.2e-189;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                         681 TGGCATAAATATCTCACTCGCAATCAAAT 709
                                                                                                                                                                                                                                                                                                                                                                                                       29 TGGCATAAATATCTCACTCGCAATCAAAT 1
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Unpublished (1999)
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Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 660)
                                                                                                                                                                                                                                                                                                                                                     Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (Buropean Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                              Ansorge, W., Benes, V., Krieger, S., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No ri sequence available.
This clone (DKFZp4341102) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERNANY; Email: clone@rzpd.de.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAAACGCGGGAAAAAGTGGAAGGCGGCGA
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/lab_host="DH10B"
/clone_lib="434 (synonym: hte83)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
               DKFZp434I102_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I102_3', mRNA sequence.
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/db_xref="taxon:9606"
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/tissue type="testis"
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Unpublished (1999)
                                                                             AL044483.1 GI:5432701
                                                                                                                       Homo sapiens (human)
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                                                                                                                       surface seawater using were isolated from 200 liters of surface seawater using a combination of differential. Illitration and density-dependent gradient centrifugation. Linker-amplified shotgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating dsDNA linkers to the ends, and amplifying the fragments using Vent DNA polymerase. The resulting fragments were ligated into the pSWART vector and electroporated into MC12 cells (Lucigen; Middleton, W1)"
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/mol_type="genomic DNA"
/db_xref="taxon:186617"
/clone="$1051p3366L"
/clone lib="Scripps Pier (La Jolla, CA) uncultured virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                    /note="Marine viruses were isolated from 200 liters of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 GCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTC
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Pred. No. 9.5e-189;
0; Mismatches 7; Indels
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Best Local Similarity 98.9
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Hordeum vulgare
Hordeum vulgare
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Sporideae; Triticeae; Hordeum.
1 (bases 1 to 624)
Varshney, R.K., Zhang, H., Burton, R., Stein, N., Langridge, P. and
                                                                                                                                                                                                                                                                                                                                                                                                          161 CCGGCGTTATTTCTTGATGTCTCTGACCAGACACCATCAACAGTATTATTTTCTCCCAT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                            629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 ATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCCGTCGCAAATTGTCGCGGCGATT
                                                                                                                                                330 AAAICTCGCGCCGATCAACTGGTGCTGCGTGGTGGTCGATGGTAGAACGAAGCGGC
                                                                                                                                                                                                                                                                           CCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCAT
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Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensestr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             630 CIGITAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCG 670
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    624
    organism="Hordeum vulgare"

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/db_xref="GAB1:555471"
/db_xref="Raxon:4513"
/clone="HH07B20"
/tissue_type="coleoptile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barley ESTs from coleoptile tissue Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: stein@ipk-gatersleben.de
Insert Length: 624 Std Error:
Plate: 7 row: B column: 20
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BJ063872 NIBB Mochii normalized Xenopus tailbud library Xenopus
240 AIGITCCGGCGTIAITICTIGAIGICTCTGACCAGACACCCATCAACAGTAITAITICT 181
                                                                     685 ATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTG 744
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                                                                                                                                                       62
                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Ambibloi, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus, Xenopus.

1 (bases 1 to 641)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 GTAACGITATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACCGTTTTCCCGGGTG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
                                               CCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAA
                                                                                                                                     30 CGCGGIATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGAATGTGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          641 CGCGGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGAATGTGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mrn.yrus" rectal
/db_xxef="taxon:8355"
/clone="XL077k02"
/tisuuc_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
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19.4%; Score 641; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.3e-178;
Matches 641; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mashima, Shizuoka 411-8540, Japan
1181 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .641
/organism="Xenopus laevis"
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Location/Qualifiers
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BJ063872/c
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                                                               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); sequenced by Qiagen within the cDNA
sequencing consortium of the German Genome Project. rl sequence
also available.
                                                                                                                                                                                     6, 14059
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                                                                                                                                                                                                                                                                                                                    /tissue_type="testis"
/dev stage="adult"
/dev stage="adult"
/dev stage="bH108"
/clone lb=434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                  This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de.
Location/Qualifiers
1. 794
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                             18.5%; Score 612; DB 1; Length 794; 99.7%; Pred. No. 1e-169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp434B075"
   et al.)
 EST (Duesterhoeft, Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.7
Matches 634; Conservative
                                   Contact: MIPS
MIPS
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Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
/dev_stage="coleoptile, 1 day old"
/lab_host="DH10B"
/clone lib="HH"
/note="Vector: pSPORT; Site_1: SalI (5-end of cDNA);
Site_2: NotI (3-end of cDNA); bue to the cloning system used blue-white selection for recombinants is not 100 % reliable. Average insert size is 1:3 kb."
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                                                                                                                                                   Score 615.8; DB 6; Length 624;
Pred. No. 7e-171;
0; Mismatches 2; Indels 0;
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Matches 617; Conservative 0
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2414 AAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATC 2473
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Biology Dept.
Biology Dept.
San Diego State University
5500 Campanile Dr, San Diego, CA 92102, USJ
Tel: 6195941336
Fax: 61959576
Email: forest@sunstroke.sdsu.edu
Class: shotgun.
                                                                                                                                                                                                                     AGACTGTCGATGAAGCCCTGAAAGCCCCCGCAGACT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; environmental samples. 1 (bases 1 to 608)
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99.7%;
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                                    CL655575 172 bp DNA linear GSS 09-JUL-200.
PR10124a_C01 - PR10124a.B21 (752) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
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                                                                                                                                                                                                                                   Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppabB: an AcedB database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                              end
                                                                                                                                                   Pristionchus pacificus
Pristionchus pacificus
Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Neodiplogasteridae, Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                 Fax: "Carly". real. commercetuebingen. mpg.de
This library was generated at Caltech, Pasadena, USA and
sequenced at Vancouver, Canada.
Seq primer: Tractouver, Canada.
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                                                                                                                                                                                                                                                                                                                      Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Fax: 00497071601391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 752
Organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3%; Score 603; DB 9; Lilarity 98.9%; Pred. No. 4.7e-167; Conservative 0; Mismatches 5;
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                                                                                                                     CL655575.1 GI:50134897
                                                                                      survey sequence.
CL655575
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Matches 628; Conserv
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CACGIATTGCCGCCACATGGAAAACGCCCCAGAAAGGTGAAATCATGCCGAACATCCCGC 2533
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272 CACGTATTGCCGCCACCATGGAAAACGCCCAGAAAAGGTGAAATCATGCCGAAACATCCCGC 213
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/mol_type="genomic DNA"
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/db clone="SIO51g3D4L"
/clone="sIO51g3D4L"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Mead, D., Azam, F. and Rohwer, F. Genomic analysis of uncultured marine viral communities Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY080094
AY080094 Scripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3D4L, genomic survey
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Pred. No. 3.7e-163;
0; Mismatches 2; Indels 0;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2): Email 8 wiemann@dKf2- heidelberg.de;
sequenced by GBF (NRZi): Emails Research Centre for Biotechnology Ltd
Braunschweig/Germany) within the cDNA sequencing consortium of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No s1 sequence available.
This clone (DKRZp564C157) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
ACTGGGTGCCAGCGTGGTGGTGGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGC
                                                                                                                                                                                                                                                                                              CATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGAT
                                                                       GGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCGCTGGA
                                                                                                                           TGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCACTAATGTTCCAGCGTTATTTCTTGA
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                                                                                                           TGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGA
                                                                                                                                                                  TGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACT
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                                                       GGCGGTGCACATCTTCTCGCGCAACGCGTCAGTGGGCCTGATCATTAACTATCCGCTGGA
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/organism="Homo sapiens"
/mol_type="mRNA"
/db Xref="taxon:9606"
/clone="DKFZp564C157"
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EST (Bloecker, et al.)
Unpublished (1999)
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EST.
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No 81 sequence availa
This clone (DKFZp564C
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AUTHORS
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/clone lib="564 (8ynonym: hfbr2)"
/clone lib="564 (8ynonym: hfbr2)"
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                                                                                                                                                           17.8%; Score 586.4; DB 1;
99.7%; Pred. No. 3.7e-162;
iive 0; Mismatches 2;
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Job time : 6745.2 secs
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Minimum DB Maximum DB

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Sequence 61, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 10, Appl
Sequence 194, App
Sequence 194, Appl
Sequence 1, Appl
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Sequence 2, Appl
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Sequence 2, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 134.74

Sequence 136.74

Bublication No. US20030037355A1

GENERAL INFORMATION:

APPLICANT: The Scripps Research Institute

TITLE OF INVENTION: expression in plants

TITLE OF INVENTION: expression in plants

FILE REFERENCE: 27801-20014.04

CURRENT APPLICATION NUMBER: US 09/620,897

PRIOR APPLICATION NUMBER: US 09/620,897

PRIOR APPLICATION NUMBER: US 09/620,897

PRIOR PILING DATE: 2000-01-21

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 75

SEQ ID NOS: 75

SEQ ID NOS: 75
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                       US-10-263-153-40
US-10-263-153-40
US-10-263-153-25
US-10-263-153-25
US-10-263-153-26
US-10-263-153-66
US-10-263-153-15
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US-10-801-487-194
US-10-801-938-194
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US-10-313-963A-54
US-10-495-491-2
US-10-495-491-1
US-10-495-491-3
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US-10-801-486-194
US-10-801-493-194
US-10-263-153-7
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US-10-313-963A-52
US-10-671-995A-2
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100.0%; Score 3300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3300; Conservative 0; Mismatches
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 LENGTH: 3300
1462.4
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Sequence 18,
Sequence 17,
Sequence 16,
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(ggn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
(cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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Compugen Ltd.
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US-09-765-555-15

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US-09-765-555-16

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US-10-257-184A-1

US-10-149-472-5
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             GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
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100.0
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97.2
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Perfect score:
Sequence:
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Sequence 52, Appl Sequence 2, Appli Sequence 1, Appli Sequence 32, Appl Sequence 32, Appl Sequence 2, Appli

GENERAL INFORMA Sequence 1, A Sequence 2, A Sequence 19, ö

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Result

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US-09-765-555-15
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                        RESULT 2
US-09-765-555-15
Sequence 15, Application US/09765555
Publication No. US20030037355A1
GENERAL INFORMATION:
APPLICANT: The SCTIPPS Research Institute
TITLE OF INVENTION: Methods and compositions to mod;
TITLE REFERENCE: 27801-20014.40
CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 09/620,897
PRIOR PELING DATE: 2000-01-21
PRIOR PELING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 3300
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ORGANISM: Artificial Sequence
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Matches 3300; Conserv
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TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220
                                                                                              GAAGCGGTDAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
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OTHER INFORMATION: Parial sequence of pMal-Ap3 and zinc finger

OTHER INFORMATION: protein ZFPAp3
US-09-765-555-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-09-765-555-18
Sequence 18, Application US/0976555
Fublication No. US20030037355A1
GENERAL INFORMATION:
TITLE OF INVENTION: Methods and compositions
TITLE OF INVENTION: expression in plants
TITLE OF INVENTION: expression in plants
CURRENT APPLICATION WUMBER: US/09/765,555
CURRENT FILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 18
LEMOTER 13300
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ORGANISM: Artificial Sequence
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FILE OF INVENTION: expression in plants FILE REFERENCE: 27801-20014-40  CURRENT APPLICATION NUMBER: US/09/765,555 CURRENT FILING DATE: 2002-05-24  PRIOR FILING DATE: 2000-01-21  PRIOR FILING DATE: 2000-01-21  PRIOR FILING DATE: 2000-01-21  NUMBER OF SEQ ID NOS: 75  SOFTWARE: FastSEQ for Windows Version 4.0  SEQ ID NO 17  LENGTH: 33.00  TYPE: DNA  ORGANISM: Artificial Sequence FEATURE:  COTHER INFORMATION: Partial sequence of pMal-m4 and zinc finger  OTHER INFORMATION: protein ZFPm4  US-09-765-555-17	Query Match         97.4%;         Score 3215.2;         DB 10;         Length 3300;           Best Local Similarity         98.4%;         Pred. No. 0;         5;         Indels         0;         Gaps           Matches 3247;         Conservative         0;         Mismatches         53;         Indels         0;         Gaps           1         CGGACACCATCGAATGGTGAAACCTTTGGCGGTATGGCATGATAGCGCCCGGAAGAGA         1         CGGACACCATCGAATGGTGAAAACCTTTGGCGGTATGGCATGATAGCGCCCGGAAGAGA           0         GTCAATTCAGGCTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG         61         GTCAATTCAGGCTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG           1         GTCAATTCAGGCTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG         61         GTCAATTCAGGCTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCGAGAGTATGCCGAGAGTATCCGCAGAGTATGCCGAGAGTATACCCAGAGTATCCGCAGAGTATGCCGAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATCCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATACCCAGAGTATCCCCAGAGTATACCCAGAGAGTATACCCAGAGAGTATACCCAGAGAGTATACCCAGAGAGTATACCAGAGAGTATACCCAGAGATACCAGAGAGTACCAGAGAACACAC	0y         121 GTGTCTTTATCAGACCGTGGTGAACCAGGCCAGCCAGCCA	301 AGGGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG  361 TGGTGGTGCTGGTGGTGGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCAATC  421 TTCTCGCGCAACGCGTCAGTGGCTGATCATTAACTATCCGCTGGATGAAGCGGCGTGCAATC  421 TTCTCGCGCAACGCGTCAGTGGCTGATCATTAACTATCCGCTGGATGACAGCTGCAAGCGATGCCA  421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGCCA  421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCTTGATGCCTTGACCAGA  481 TTGCTGTGGAAGCTGCCTGACTAATTCTTCATGTCTTGACCAGA  581 TTGCTGTGGAAGCTGCCTGACTAATTCTTCAATGTCTTTGACCAGA  681 TTGCTGTGGCAACGCTCACTAATGTTCCTGACCAGA  681 TTGCTGTGGAAGCTGCCTGACTAATGTTCCTTGATGTCTTTGACCAGA  681 TTGCTGTGGAAGCTGCCTGACTAATGTTCCTTGATGTCTTTGACCAGA  681 TTGCTGTGGAAGCTGCCTGACTAATTTCTTTAATGTCTCTGACCAGA  681 TTGCTGTGGAAGCTGCCTGACTAATTTCTTTAATGTCTCTGACCAGA  681 TTGCTGTGGCAAGCTGCCTGACTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGCCTGACTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGCCTGACTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGACTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGCCTGACTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGACTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGCCTGACTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGACTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGACTAATTTCTTTAATTTCTTTAATGTCTCTTGACCAGA  681 TTGCTGTGCCTGAAGCTGACTAATTTCTTTAATTTCTTTAATTTCTTTAATTTCTTTTTT	541 CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC [

Qy         2941 AAGTCTTTCTCTCGGTCTGACATCTCGTCCGGCACCAACGTACTCACCACCGGGGAAAG 3000           Db         2941 AAGTCTTTCTCTCGGTCTTGCGAGCACCAACGTACTCACCACGGGGAAAG 3000           Qy         3001 CCCTATGCTTGTCGGAATGTGGTAAGTCCTTCAGCGCACGATACCTGGTGCGCCAC 3060           Db         3001 CCCTATGCTTGTCCGGAATGTGGTAAAGTCCTTCTCAGAGGTCTCACTGGTGCGCCAC 3060           Qy         3061 CAGCGTACCCACACGGTGAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTAGC 3120           Db         3121 CAGCGTACCCACACGGTGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGC 3120           Qy         3121 CAGCGGACCCACCAGGGTGAAAAACCGTATAAAATGCCCAGAGTGCGGCAAATCTTTTAGC 3120           Db         3121 CAGCGGACCCACCAGCGCAGCCATCAAAAGCCTATAAAATGCCCAGAGTGCGGCAAATCTTTTTAGC 3120           Cy         3121 CAGCGGACCCACCGGCCCATCAACGCACTCATACAAAATGT 3180           Cy         3181 CCAGAATGGCCAGCCATCAACGCACTCATACTGGCGAGAAGCCATACAAATGT 3180           Cy         3181 CCAGAATGGCCAGCCAGCCCACCACCACACTCATCCGGAAAGCCATACAAATGT 3180           Cy         3181 CCAGAATGTGGCCAACTTTCTCTCTCAACCTCACACGTACCAACGTACTCAC           CAGGTAAAAAACTAGTGGCCAGCCCAGCCCAGACCCGTACCAACGTACCAACGTACTCAC           CAGGTAAAAAAAACTAGTGGCCAGCCCAGACCCGTACCGTACCAACGTACCACACCTACCACCTACACCTACACCTACCACACCTACACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCTACACCAC	NESULT 5  19.09-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-555-16  19.00-765-765-765-765-765-765-765-765-765-765
1861   GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920   1861   GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920   1921   GAGATCCGGCGTGATATTATAACAAGATCTGCTGCCGAACCCGCCGAAAACCTGGGAA 1920   1921   GAGATCCCGGCGCTGATATCAACTGAAGCGTAAGACGCGCTGATGTTCAAC 1980   1921   GAGATCCCGGCGCTGATAAAAACTGAAAGCGAAAGCTAAGAGCGCGCTGATGTTCAAC 1980   1931   CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGCGCTGATGTTCAAC 1980   1931   CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGCGCTAAGCTCAAGCTCAAGCTCACTTCACCTGGCCGCTGATTGCTGCTGACGCGCGCAAAGC 2040   1931   TATGAAAACGGCAATTAAAGACGTGGCTGGTTGCTGCTGGCGCGCGAAAGC 2000   1941   1141	2221   GCATGGTCCAACATCGACACCAGCAAGTAATTATGGTGTAACGGTACTGCCGACCTTC   2280

1381   CTGGCAMATATCTGAMATGAGCTGTTGACMATAATCTGGGCTGGTTAATGTGGGA 1440   1131   CTGGCAMATATCTGGAMATGAGCTGTTAGCGTGTTAGCTGGTTTAGCTGTTTTCAGCA 1540   1441   MTTGGAGGGGGTAATCTGGAATAATCTGGTAATTCTGGAGGTGTTTTCAGCA 1540   1441   MTTGGAGGGGGTAATCTGGTAATTCGGTGTTTTCAGCAATTCTGGAGGTGTTTTCAGCA 1540   1441   MTTGGAGGGGGTAATCTGGTAATTCGG 1560   1540   GCGCTTGACGCGGTTAATCTGGTAATTCGGTGTTTTCAGCAATTCGTAATTCGGAGGTGTTAGCTGTTTTCAGCAATTCGTAATTCGGAGGTGTGTGT
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                                                                                                                                                                                                                            FEATURE:

NAME/KEY: CDS

LOCATION: (1528)..(3453)

OTHER INFORMATION: /product = fusion protein MBP Cystatin C BMP-PEATURE:

NAME/KEY: misc feature
LOCATION: (2689)

OTHER INFORMATION: (Amino acid sequence)
FEATURE:
NAME/KEY: misc feature
LOCATION: (3067)..(3108)

OTHER INFORMATION: /spacer between Cystatin C andBMP-2
FUBLICATION INFORMATION: /bpacer between Cystatin C andBMP-2
FUBLICATION INFORMATION: /bpacer between Cystatin C andBMP-2
FUBLICATION INFORMATION: /ppacer between Cystatin C andBMP-3
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DATABASE ENTRY DATE: 2001-05-07
RELEVANT RESIDUES: 1528 - 3453
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99.2%; Pred. No. 0;
iive 0; Mismatches 22; Indels
                                                                                                                                                                                                           OTHER INFORMATION: Expression vector pMalc2cchbmp2
                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Matches 2719, Conservative
             SOFTWARE: Patentin Ver.
SEQ ID NO 1
LENGTH: 7373
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Publication No. US20040087524A1
GENERAL INFORMATION:
APPLICANT: Maubach, Gunter
ITLE OF INVENTION: Agent for postoperative use
FILE REPERENCE: 2945-101
CURRENT APPLICATION NUMBER: US/10/257,384A
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: PCT/DE 01/01510
PRIOR PILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 19
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                                         CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC
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                                                                                                                              APPLICANT: GOUBIN-GRAMATICA, FRANCOISE
APPLICANT: DUCOMMUN, BERNARD
APPLICANT: DUCOMMUN, BERNARD
APPLICANT: DUCOMMUN, BERNARD
APPLICANT: DUCOMMUN, BERNARD
TITLE OF INVENTION: WETHOD FOR OBTAINING HUMAN CDC25 PHOSPHATASES AND METHOD
TITLE OF INVENTION: FOR IDENTIFYING HUMAN CDC25 PHOSPHATASE MODULATORS
TITLE OF INVENTION: FOR IDENTIFYING HUMAN CDC25 PHOSPHATASE MODULATORS
TITLE OF INVENTION: FOR IDENTIFYING HUMAN CDC25 PHOSPHATASE MODULATORS
FILE REFERENCE: DAM - 206-06-07
FILE REPERSENCE: 2000-06-07
FILE REPERSENCE: 2000-012-13
PRIOR PLILING DATE: 2000-12-13
PRIOR PLILING DATE: 1999-12-14
PRIOR PLILING DATE: 1999-12-14
PRIOR PLILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-05-30
PRIOR FILING DATE: 2000-09-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PACENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Synthetic COTHER INFORMATION: UM109 / PMAL - Hs Cdc25C strain US-10-149-472-5
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GGATCCTCCAGICCCGGCAAGCCGCCGCGCGTGGGAGG 2741
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82.0%; Score 2705.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2707; Conservative 0; Mismatches
                                                               US-10-149-472-5; Sequence 5, Application US/10149472; Publication No. US20040029204A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
2701
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Publication No. US20040110161A1
GENERAL INPORMATION:
FRIED TITLE OF INVENTION: Method for detecting mute;
TITLE OF INVENTION: Method for detecting mute;
TITLE OF INVENTION: mucleotide sequences;
TITLE REFRENCE: 612, 406-033
CURRENT APPLICATION NUMBER: US/10/343,859
FRIOR APPLICATION NUMBER: DO19-11-24
FRIOR FILING DATE: 2001-10-13
FRIOR FILING DATE: 2000-08-04
FRIOR FILING DATE: 2000-08-
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                                                                                                                                                                                                                                                                           ; TYPE: DNA; ORGANISM: Artificial sequence; PEATURE:
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: pWALc2x-mutS
US-10-343-859-9
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                               SQUENCE 9, Application US/10343859
| Publication No. US20040110161A1 |
| GENERAL INPORMATION: APPLICANT: NATURE OF INVENTION: Method for detecting mut: TITLE OF INVENTION: MUMBER: US/10/343,859 |
| CURRENT FILING DATE: 2003-11-24 |
| PRIOR FILING DATE: 2001-07-13 |
| PRIOR FILING DATE: 2001-07-13 |
| PRIOR FILING DATE: 2000-08-04 |
| NUMBER OF SEQ ID NOS: 52 |
| SEQ ID NO 9 |
                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Score 2698;
Pred. No. 0;
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99.8%;
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Matches 2701; Conservative
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            RESULT 9
US-10-343-859-9
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abbort Laboratories
APPLICANT: Abbort Laboratories
APPLICANT: Maine, Gregory T.
APPLICANT: Patel, Chandu B.
APPLICANT: Patel, Chandu B.
APPLICANT: Patel, Chandu B.
TITLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REFERENCE: 6949. US. O.
CURRENT FILING DATE: 2002-10-22
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                      Length 7112;
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                                                                                                                                                                                                                                                                                                                      DB 18;
                                                                                                                                                                                                                                                                ; LOCATION: (1528)...(3189)
; OTHER INFORMATION: pMBP-c2X-ToxoP30dell1 (52-214aa)
US-10-263-153-40
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; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                   81.5%;
                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Toxoplasma gondii
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Matches 2694; Conservative
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RESULT 10 US-10-263-153-40 ; Sequence 40, Application US/10263153

1711   GCTCANTCTGGCTGTAGATCACCCGGACAAACCGTATTACTTACCTACGGCTGTT 1860	; Sequence 30, Application US/10263153 ; Publication No. US20040067239A1 ; GENERAL INFORMATION: ; APPLICANT: Abbott Laboratories ; APPLICANT: Maine, Gregory T. ; APPLICANT: Patel, Chandu B. ; APPLICANT: Ginsburg, Sanford R. ; APPLICANT: Bliese, Timothy R.
CCCAPTCTGGCTTCTGGCTTGGCTTGGCTTGGCANTTCACCAGCTCGCANTCTCGTGGCANTCTGGTTGGTTGGTTGGCTTGGC	1621 ACCGGAATTAAAGTCACCGTTCAACCGGATAACTCGAAGAGAATTCCCACAGGTT 1680 1681 GCGGCAACTGGCGGTTATCTTCTGGGCACGCCTTTGGTGCTAC 1740 1681 GCGGCAACTGGCGGATGGCCCTGACATTATCTTCTGGGCACGACGGCTTTGGTGGTCGCTAC 1740 1681 GCGGCAACTGGCGGATGGCCTGACATTATCTTCTGGGCACGACGGCTTTGGTGGTCGCTAC 1740 1741 GCTCAATCTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800 1741 GCTCAATCTGGCTGTTGGCTGAAATCACCCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800

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TITLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REFERENCE: 6984.US.01
CURRENT APPLICATION NUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PASESEQ for Windows Version 4.0
LENGTH: 7259
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// NAME/KEY: CDS

// LOCATION: (1528)...(3336)

// OTHER INFORMATION: pMBP-c2x-ToxoF30de14de18 (83-294aa)
US-10-263-153-30
                                                                                                                                                                                                                                           DB 18;
                                                                                                                                                                                                                                        Score 2690.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.8%;
Matches 2694; Conservative
                                                                                                                          TYPE: DNA ORGANISM: Toxoplasma gondii
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    i LOCATION: (1528)...(3399)
    j OTHER INFORMATION: pMBP-c2X-ToxoP30dell0 (52-284aa)
    US-10-263-153-35

                                                                                                                                                     Score 2690.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                     Query Match
Best Local Similarity 99.8%;
Matches 2694; Conservative
SEQ ID NO 35
LENGTH: 7322
TYPE: DNA
ORGANISM: TOXODlasma gondii
FEATURE:
                                                                              NAME/KEY: CDS
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 Squence 35, Application US/10263153
Squence 35, Application US/10263153
Publication No. US20040067239A1
GENERAL INFORMATION:
APPLICANT: About Laboratories
APPLICANT: Maine, Gregory T.
APPLICANT: Patel, Chandu B.
APPLICANT: Ginsburg, Sanford R.
TITLE OF INVENTION: GENERICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REFERENCE: 6984.US.Ol
CURRENT APPLICATION NUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
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1991 CTGCAAGAACGGTACTTCACCTGGCCGCTGATTGCGCGGGGTTATGCGTTCAAG 2040     1912 CTGCAAGAACGGTACTTCACCTGGCCGCTGATTGCGTGGGGGGTTATGCGTTCAAG 2040     2041 TATGGAAACGGCAAGTACGACATTAAGACGTGGGGGGTTAACGCTGGCCGCAAGCG 2100     2041 TATGGAAACGGCAAGTACGACATTAAGACGTGGGCGGTGGATTACGTGGCCGCGAAGCG 2100     2041 TATGGAAACGGCAAGTAGCACATTAAGACGATGGATGCCGCGCGCG	RESULT 13 US-10-263-153-25  Sequence 25, Application US/10263153  Sequence 25, Application US/10263153  Sequence 25, Application No. US20040067239A1  SENDICATION OF USCO040067239A1  APPLICANT: About Laboratories  APPLICANT: Maine, Gregory T.  APPLICANT: Patel, Chandu B.  APPLICANT: Patel, Chandu B.  APPLICANT: Bliese, Timothy R.  TITLE OF INVENTION: GENETICALY ENGINEERED P30 ANTIGEN,  TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF  FILE REFERENCE: 698-US.01  CURRENT FILING DATE: 2002-10-22  NUMBER OF SEQ ID NOS: 74  SOFTWARE: FastSEQ for Windows Version 4.0  SOFTWARE: FastSEQ for Windows Version 4.0  SOFTWARE: TASE  TYPE: DNA  ORGANISM: Toxoplasma gondii  FEATURE:  NAME/KEY: CDS  LOCATION: (1528)(3429)
901 ACGRITACCGARGACAGCTCATGTTATATCCCGCCGTTAACCACCACCACAGAGGATTTTC 960 901 ACGRITACCGARGACAGCTCATGTTATATCCCGCCGTTAACCACCACCACCACAGGGATTTTC 960 901 ACGRITACCGARGACAGCTCATGTTATATCCCGCCGTTAACCACCACCACCACGGGGTTA 1020 902 GCCTGCTGGGGCAAACCAGCTGAACCACCTCTGCACCACCACCACGGGCGGTGA 1020 1021 AGGGCAATCACTCTTGCCCGTTCACTCGTGAAAAAACCACCTGGCGCCACATA 1080 1021 AGGGCAATCAGCTGTTGCCCGTTCACTGTGAAAAAAAACCACCTGGCGCCCAATA 1080 1031 AGGGCAATCAGCTGTTGCCCGTTCACTGTGAAAAAAAAACCACCTGGCGCCCAATA 1080 1041 CCCGACTGGAACCGCTCTCCCCGGCGCTTGCTGTAAAAAAAA	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGGAA

, OTHER US-10-263	; OTHER INFORMATION: pMBP-c2X-ToxoP30del4C (52-294aa) US-10-263-153-25	qa i	GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 102
Query M. Best Loc Matches	Query Match  81.5%; Score 2690.4; DB 18; Length 7352; Best Local Similarity 99.8%; Pred. No. 0; Matches 2694; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	à a	AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCCCCTGGCGCCCAATA 
QY Dp	1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60 	Qy Dp	CGCAAACGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACGGTTT 
& g	61 GTCAATTCAGGGTGGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120 	y da	
& 48		S G	1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCCAATGCTTCTGGCG 1260 
oy Dp	GGCAC   GGCAC	oy GB	1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320 
\$ 8 8	241 AACAACTGGCGGGCAAACAGTCGTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC 300 241 AACAACTGGCGGCAAACAGTCGTTGCTGGTTTGGCGTTGCCACCTCCAGTCTGGCCTTGC 300	S G	1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 1380 
& 8	ACGCGCCGTCGCAAATTGTCGCCGCGATTAAATCTCGCGCCGATCCACTGGGTGCCAGCG	QQ QQ	1381 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440 
& 8	TGGTGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATC	Qy Dp	1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 
<u>\$</u> 8	TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCATTCTCGCCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGAACAGAGGGGGAAGCGAACAGAGGGGGGAACAGTGGGAACAGTGAGCAATGAGGATGAGGATGAGGATGAGGATGATCAATTAACTATCAGATGAACAGAGAGGGGGAAGAGAACAGATGAGGAACAGATGAGAACAAGATGATCAATTAACTATCAGATGAACAGAGAGGAGGAACAATGATCAATAACAACAAGAACAGAAAACAGAATGAGAACAAGATGAACAATAAT	Ογ Db	1501 GCACTTCACCAACAAGGACCATAGATATGAAAACTGAAGAAGGTAAACTGGTAATCTGG 1560 
රු සි	TTGCTGTGGAAGTTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA	oy op	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGT 1620 
· & 8	CACCONTCAACAGTATTATTTCCCATGAAGACGGTACGCGACTGGGCGTCGACGCTCCATGAAGACGGTACGCACTGGGCGTCGTACCCATGAAGACGGTACGCGACTGGGCGTACGCATACTGAAGACGGTAACGGTAACGGTAACGCATAACGCATAAGAAGGGTAACGCATAACGCAACGGTAACGCAACGGTAACGCAACACGCAACGCAACACGCAACACGCAACACGCAACACGCAACCAACACACACAACA	& 8	1621 ACCGGAATTAAAGTCACCGTTGAGCATCGGATAAACTTGGAAGAAATTCCCACAGGGTT 1680 
\ \dots \text{8}	TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAAGCTGCTCGGTCGCGTTTAAGTTCTGTCTCGGTTTTAAGTTTCTGTTCTGGTTTTAGGTCGCGTTTAAGTTCTGTCTCGGTTTTAGGTCGCGTTTAAGTTCTTCTTCGGTCGTTTAAGTTCTTCTTCGGTCGTTAAGTTCTTCTTCGGTCGTTAAGTTCTTCTTCGGTCGTTCGT	Oy Dp	1681 GCGCCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACGGCTTTGGTGGCTAC 1740
<i>&amp;</i> 8	CGCGTCTGCGTCTGGCTGGCTGGCTAAATATCTCACTCGCAATCAAT	Qy	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT 1800 
& 8	CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCACAAACCATGCAAATGCTGAACGGGAAACGGGAAACGGAAATGCTGAATGCTGAACGGGAAACGAAAGAATGCCATGTCCCATGTTTTAACAACAACAACAACAAACA	Qy Dp	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 
<i>&amp;</i> 8		Qy Dp	1861 GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 
5 8	TGGGGGCCATTACGAGTCCGGGCTGCGCTTGGTGCGGATATCTCGGTAGTGGGATACG 	QV GD	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGGCGCGCTGATGTTCAAC 1980 
<i>&amp;</i> 8	ACGATACCGAAGACAGCTCATGTTATATCCCGCGTTAACCACCATGAACAGGATTTTC	y d	1981 CTGCAAGAACCGTACTTCACCTGGCGGCTGATTGCTGCTGATGGGGGGGTTATGCGTTCAAG 2040
ł <i>ò</i>	GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAA	QQ QD	2041 TATGAAACGCCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100 

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		Db   1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG			Oy         1501 GCACTTCACCAACAAGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG         1501 GCACTTCACCAACAAGAGCATATGAAAATCGAAGAAGGTAAACTGGTAATCTGG         1501 GCACTTCACCAACAAGAGCATATGAAAATCGAAGAAGGTAAACTGGTAATCTGG         1500	QY         1561 ATTAACGGCGATAAAGGCTATAACGGTCCGCTGAAGTCGGTAAGAATTCGAGAAAGAT 1620           DD	Y 1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680	1681	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT	/ 1801 CCGTTTACCTGGGATGCCGTACGTACAAGCTGGATGCTTACCCGATCGCTGTT 1860	1861 GAAGGGTTATCGCTGATTTATAACAAAGATCTGCCGAACCGGCGAAAAACCTGGGAA 1920 	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGGGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980 1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040	2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100	2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC 2160 [	2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220 		2340
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Oy 2341 CCGAACAAAGAGTTCGTTGGTGGCGTGCTGAGGTATTAACGCCGCCAGT 2340

Db 2341 CCGAACAAAGAGTTCCTCGAAAACTATCTGCTGATGAAGGTCTG 2400

2401 GAAGGGGTTAATTAAAGACAAACGGTTCCTCGAAACTATCTGCTGATGAAGGTCTG 2400

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Oy 2401 GAAGCGGTTAATTAAAGACAAACCGCTGGGTGCCGTGACGCTGAAGTCTTACGAGGAAGG 2460

Db 2401 GAAGCGGTTAATTAAAGACAAACCGCTGGGTGCCGTGAAGTCTTACGAGGAAGG 2460

Oy 2461 TTGGCGAAAGATCCCACTATTGCCGCCACTGGAAAGTCTTACGAGGAAGG 2520

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Oy 2521 CCGAACATCCCACAATTGCCGCTATTGGAAAACGCCCAGAAAGGTGAAATCATG 2520

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Perfect score:
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Sequence 7, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 213, App Sequence 213, App Sequence 213, App Sequence 214, App Sequence 254, App			Length 7475;
US-09-503-222-7 US-08-125-462-2 US-08-891-848-2 US-08-891-848-5 US-09-125-462-5 US-09-128-314-4 US-09-056-556-213 US-09-072-567-213 US-09-06-43-69-9 US-09-643-69-9 US-09-643-69-9 US-09-643-69-848-48-69-9 US-09-643-69-848-69-9 US-09-643-69-649-69-69-69-69-69-69-69-69-69-69-69-69-69	MENTS	Derivatives Inc.  Sos0, Version #1.25036 4430/073	2700; DB 2; L
US-09-50 US-08-12 US-08-12 US-08-12 US-08-12 US-09-12 US-09-05 US-09-05 US-09-07	ALIGNMENT		Score
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100.0%; Pred. No. v,
... 0; Mismatches
REFERENCE/DOCKET NUMBER: RAN 4430/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 235-4387
TELEPRA: (973) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7475 base pairs
                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Simi
Matches 2700;
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US-09-096-570-1
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                                   GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
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                   TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
                                                                                   GCATGGTCCAACATGGACACCCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
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COUNTRY: N.J.

ZIP: N.J.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,570
FILING DATE:
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Sequence 1, Application US/09096570

APPLICANT: Atwood, Michael R

APPLICANT: Hurst, David N

APPLICANT: Way, Paul B

APPLICANT: Raynham, Tony M

APPLICANT: Raynham, Tony M

APPLICANT: Wilson, Francis X

TITLE OF INVENTION: Amino Acid Derivatives

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/971,036
FILING DATE:
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NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 38522
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1921   GAGATCCCGGCCCTGATAAAGAACTGAAAGCGAAAGCGCCCTGATGTTCAACCCCTGATGTCAACCCGCTGATGTCAACCCGCCTGATGTCAACCCGCCTGATGTCAACCCGCCTGATGTCAACCCGCCTGATGTCAACCCGCCTGATGTCAACCCGCCTGATGTCAACCCGCCTGATGTCAACCCGCCTGATGTCAACCCGCCTGATGCCTTCAACCCGCCGAAACCCGCCGAAACCCGCCGAAACCCGCCG	RESULT 3 US-09-265-617B-1   Sequence 1, Application US/09265617B   Patent No. 6372883   Patent No. 6372883   GENERAL INFORMATION:   APPLICANT: Attwood, Michael R.     APPLICANT: Attwood, Michael R.     APPLICANT: Hulling Philip S.     APPLICANT: Ray, Paul B.     APPLICANT: Ray, Paul B.     APPLICANT: Ray, Paul B.     APPLICANT: Aptham, Tony M.     TITLE OF INVENTION: Antiviral Medicaments     TITLE OF INVENTION: Antiviral medicaments     CURRENT FILING DATE: 1999-03-10     PRIOR APPLICATION NUMBER: GB9806615.8     PRIOR APPLICATION NUMBER: GB9806330     NUMBER OF SEQ ID NOS: 24     SOFTWARE: PatentIn Ver. 2.0
## ## ### ##########################	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT   1680   1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT   1680   1681 GCGGAACTTAAACTCCGGATCGCACACGTT   1680   1681 GCGCCAACTGGCGATGGCCTTGACTTTCTCGGGCCACACGACCGCTTTGGTGGCTAC   1740   1681 GCGCCAACTGGCGTTGGCTGAATTCTTCTCGGGCACACGACCGTTTGGTGGCTAC   1740   1741 GCTCAATCTGGCCTGAATCACCCCGGACACACGACCGTTAT   1800   1741 GCTCAATCTGGCTGATGGCTTACACGCCACACGACCGACC

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                                                                                                                                                                                                                                         LENGTH: 5926 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular

MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "pEM delta R.adj to 1"
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43.0%; Score 1417.6;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1455; Conservative 0; Mismatches
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 5789-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 420 2205
TELEFAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-027-169-3
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CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040
                                                                                                                 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100
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TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
TITLE OF INVENTION: ATP-DEPENDENT TRANSPOSITION PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Brown (Alston & Bird, LLP)
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,169
FLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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CTY: Raleigh STATE: NC COUNTRY: USA ZIPP: 7608
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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; Patent No. 6420524
; GENERAL INFORMATION:
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                                                               866 GACACCATCGAATGGCGCAAAACCTTTCGCGGTATGGTGATGATAGCGCCCGGAAGAGAGT
                                                                                                                926 CAATTCAGGGTGGTGGTGAATGTGAAACCAGTAAAGGTTATACGATGTCGCAGAGTATGCCGGT
                                                                                                                                                                   986 GTCTCTTATCAGACCGTTTCCCGCGTGGTGAAACG
                                                                                                                                                                                                      CGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACAA
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GENERAL INFORMATION:

APPLICANT: Hall, Barry G.

TITLE OF INVENTION: METHOD OF DETERMINING EVOLUTIONARY POTENTIAL OF MUTANT

TITLE OF INVENTION: EFFICACY

TITLE OF INVENTION: EFFICACY

FILLS REFERENCE: 1766/60851

CURRENT APPLICATION NUMBER: 06/149,813

PRIOR FILLING DATE: 2000-08-18

PRIOR PILLING DATE: 1099-08-19

PRIOR PILLING DATE: 1099-08-19

PRIOR PILLING DATE: 1099-08-19

PRIOR PILLING DATE: 1090-08-19

PRIOR APPLICATION NUMBER: 60/149,813

PRIOR PILLING DATE: 1099-08-19

SOFTWARE: PatentIN Ver. 2.1

SOFTWARE: PATENTIN Ver. 2.1

SOFTWARE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: DACSE2

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MOLECULE TYPE: other nucleic acid
ORIGINAL SOURCE:
ORGANICN: E. COLI
STRAIN: BL21 (DE3)
PUBLICATION INPORMATION:
AUTHORS: NOBLYVAT FUJII ET AL,
TITLE: FROM SAID FUSED DNA SEQUENCE, AUTHOR SAID FUSED DNA SEQUENCE AND METHOD OF
TITLE: EXPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 4557
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COMPUTER: RAINTED FORM
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/778,717
FILING DATE: 12-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 35225/1995
PTING DATE: 28-DEC-1995
ATTORNEY, AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2084-031-0
TELEPHONE: 703-413-3000
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                                                                       GGCAAATATTCT 1394
                                                                                                                      2244 GGCAAATATTCT 2255
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MEDIUM TYPE: Floppy
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Best Local Similarity
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ZIP: 22202
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US-08-487-283A-18/c
US-08-487-283A-18/c
; Sequence 18, Application US/08487283A
; Patent No. 6355245
; GENERAL INFORMATION:
; APPLICANT: Evans, Mark J.
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                                                                                                                                   Sequence 2, Application US/08148675A
| Patent No. 5506121
| GENERAL INFORMATION:
| APPLICALITY SKETTA, ATNE; Schmidt, Thomas
| TITLE OF INVENTION: STREPTAVIDIN
| TITLE OF INVENTION: STREPTAVIDIN
| TITLE OF INVENTION: STREPTAVIDIN
| TOMBER OF SEQUENCES: 2
| CORRESPONDENCE ANDRESS: ADDRESSE: Relfe & Lynch |
| STRET: 805 Third Avenue |
| CITLE OF WAY YORK City |
| STATE: New York City |
| COUNTRY: USA
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
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0; Mismatches
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Best Local Similarity 99.8
Matches 1202; Conservative
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TOPOLOGY: 1
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US-08-148-675A-2
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PCT-US96-05611A-21/C
; Sequence 21, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Lenardo. Michael J.
; APPLICANT: Matis, Louis A.
; APPLICANT: Matis, Louis A.
; APPLICANT: Meller, Elleen Elliott
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APPLICANT: Matis, Louis A.
APPLICANT: Mucller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Nother, Rocher, Russell P.
APPLICANT: Rother, Russell P.
APPLICANT: Springhorn, Joremy P.
APPLICANT: Springhorn, Joremy P.
APPLICANT: Thomas, Thomas C.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT TITLE OF INVENTION: OF INFLAMMATORY DISEASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park (Alexion)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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MOLECULE TYPE: Other nucleic acid
DESCRIPTION: DET Trc SO5/NI
DESCRIPTION: prokaryotic expression vector
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/236,208
FILING DATE: 02-MAX-1994
ATTORNEY/AGENT INFORMATION:
NAME: Seth A. Fidel.
REGISTRATION NUMBER: 38,449
REGISTRATION NUMBER: 38,449
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1776-1790
TELEFRAX: (203)776-1790
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MEDIUM TYPE: 3.5 inch, 1.4Mb storage
COMPUTER: Macintosh Cetris 610
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (203)772-3655
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 5248 base pairs
TYPE: Nucleic Acid
STRANDENNESS: Double
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Matches 1201; Conservative
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                                                                                                                                                                                                                                                            CITY: New Haven
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US-08-487-283A-18
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                                                                                     TGGTGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATC 420
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Patent No. 6821723

; BAPLICANT: AVENTIS PASTEUR

APPLICANT: Chevalier, Michel

APPLICANT: El Habib. Raphaelle

; APPLICANT: Krell, Tino

APPLICANT: Sodoyer, Regis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5; Length 5248;
APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinco, Stephen P.
APPLICANT: Squinco, Stephen P.
APPLICANT: Squinco, Stephen P.
TITLE OF INVENTION: Modified Myelin Protein Molecules NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMAURICO M. Klee
STREET: 1951 Burr Street
CITY: Pairfield
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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99.8%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                   COMPUTER: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Macintosh Centris 610
OPERATING SYSTEM: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA: PCT/US96/OS611A
FILING DATE: 02-MAY-1995
CLASSIFICATION DATA: PCT/US96/OS611A
PRIOR APPLICATION DATA: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/48,114
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 30,399
TELECOMMUNICATION INFORMATION:
TELEPAX: (203) 255 1400
TELEFAX: (203) 255 1400
TELEFAX: (203) 255 1400
TELEFAX: (203) 255 1400
TELEFAX: CARBARTERISTICS:
TENGTH TELEFAX: 5248 base pairs
                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Circular MOLECULE TYPE: Other nucleic acid DESCRIPTION: per Trc SOS/NI DESCRIPTION: prokaryotic express
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TYPE: Nucleic Acid
STRANDEDNESS: Double
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Matches 1201, Conservative
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                                                                                                                                                                                                    AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCAATA
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                                                                              ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
                                                                                                                                           GCCTGCTGGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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99.8%; Pred. No. 0;
ive 0; Mismatches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,967
FILING DATE:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger R.
REGISTRATION NUMBER: 33 055
REFERENCE/DOCKET NUMBER: P103:
TELEPHONE: 650/255-3216
TELEPHONE: 650/255-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity 99.8
Matches 1201; Conservative
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                                                                                                                                                                                                                                                                                CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
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                                                                                                                                                                                                                                                 Indels
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36.3%; Score 1199.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1201; Conservative 0; Mismatches
TITLE OF INVENTION: gp41 antigen
FILE REFERENCE: 01-1692-A
CURRENT APPLICATION NUMBER: US/10/263,103
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Petentin version 3.1
SEQ ID NO 35
LENGTH: 5312
                                                                                                                                                                   ; OTHER INFORMATION: plasmid pET-cer
US-10-263-103-35
                                                                                                                        TYPE: DNA
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
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	RESULT 13 US-09-702-705-785/c ; Sequence 785, Application US/09702705 ; Patent No. 6504010 ; GENERAL INFORMATION: ; APPLICANT: Bangur, Chaitanya S. ; APPLICANT: Lodes, Michael A. ; APPLICANT: Gary ; APPLICANT: Vedvick, Tom	APPLICANT: Carrer, Darrick  APPLICANT: Retrer, Marc  APPLICANT: Retrer, Marc  APPLICANT: Mannion, Jane  APPLICANT: Pan, Liqun  ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  ITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  ITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  CURRENT APPLICATION NUMBER: US/09/702,705  CURRENT FILING DATE: 2000-10-30  NUMBER OF SEQ ID NOS: 1833  SOFTWARE: FastSEQ for Windows Version 3.0  SEQ ID NO 785	4; Length 5502;	ACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCA 	121 GICANTICAGGGGGGGAATGTGAAACGTAACGTTATACGATGTGGGGGGGG	241 4437 301 4377	
		TGGTGGTGTCGATGGTAGACGAGGCGTCGAAGCCTGTAAGCGGCGGTGCAGCGCAGCGTGCAGCGGTGCAGCGGTGGAGCGGGGTGGAAGCGGGGGTGGAAGCGGGGGGGG	CACCCATCAACAGTATTATTCTCCCATGAAGACGGTAATTTCTTGATGTCTCTGACCAGA CACCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGACGTGGAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGAGCTGGAACAGTATATTATTCTCCCATGAAGACGGTACGCGACTGCGACTGGAGCATCTGGTCGCTCGAAATCGCGCTGCTAGCGGACTGCGACTGCGACTGCGTCGAACTCTCTCGGTTGAACATCTCTCTC	CGGAACGGAAGGCACTGCTGTTTCACTGCTGTTTACCGGACCCATTAAGTTCTGT CGCGTCTGCGTGCGTGGCATAATATCTCACTCGCAATCAAT		9970 IGUGGGGGAAGAGCGGGGCGGGGGGGGGATATCTCGGTAGTGGGATACG 3911 901 ACGATACCGAAGACCATGTTATATCCCGCGGTAACCACCATCAAACAGGATTTC 960 3910 ACGATACCGAAGCAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 3851 961 GCTGGCTGGGGAACCAGGGGACGCTTGCTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1020	ATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAACCACCTGCGGCCCAATA

CURRENT APPLICATION NUMBER: US/09/736,457   CURRENT FILING DATE: 2000-12-13   CURRENT FILING DATE: 2000-12-13   CURRENT FILING DATE: 2000-12-13   SOFTWARE: FastSEQ for Windows Version 3.0   SOFTWARE: FastSEQ for Windows Version 3.0   CCAGA 4138   SEQ ID NO 785   LENGTH: 5502   LENGTH: 5502   TYPE: DNA   CCATC 4078   US-09-736-457-785   US-09-	CTCCG 660 Query Match 16.3%; Score 1199.2; DB 4; Length 5502	NG 720         QY         1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA	Qy   61 GTCAATTCAGGGTGGAAGACAGTAACGTTATACGATGTGGAGGTATGCGGGGGGGG	AA 940 OY 121 GTGTCTTATCAGACCGTTTCCGGGTGAACCAGGCCAGCCA	Qy	TC 960 241 AACAACTGGGGGGAAACAGTGGTTGCTGATTGGGGTTGCCACCTCCAGTCTGGCCCTGC	Qy 301 ACGCGCGCGAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGCGCAGCGGCGAGGCGGCGGCGGCGGGCG	CABTR 1080  Qy 361 TGGTGGTGTCGATGGTAGRACGAGGGGTGTCGAAGCCTGTAAAGCGGCGGTGCAATC	TT 1140 QY 421 TTCTGGGGAACGGGTGGTGGTGATCATTAACTATCGGTGGATGACCAGGATGCCA	Qy	Oy         541 CACCCATCAACAGTATTATTTTCCCCATGAAGACGGTACGCGACTGGGCGTGGACACTC	Qy         601         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGCCCATTAAGTTCTGTCTCGG	Qy 661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTTCGGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATATCAGCCGATAGAATAATATCAGCCGATAGAATAATATCAGCCGATAGAATAATATCAGCCGATAGAATAATATCAGCCGATAGAATAATATCAGCCGATAGAATAGAATAATAGAGCCGATAGAATAGAATAGAATAGAATAGAATAGAATAGAGCCGATAGAATAGAATAGAATAGAGCCGATAGAATAGAATAGAGCCGATAGAAT	Qy 721 CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA	Qy         781 AIGAGGGCAICGTICCCACTGCGAIGCTGGCAACGAICGGAIGGCGCTGGGCGCGAA	Qy 841 TGCGCGCATTACCGAGTCCGGGCTGCGGCTTGGTGCGGATATCTCGGTAGTGGGAATACG
DB   4257   TTCTCGGGGAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA	601 TGGTCGCATTGGGTCACCAGCAATCGCGCTGTTAGCGGGCCCCATTAAGTTCTGTCTC 	OY 661 CGCGTCTGCGTCGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG	Qy       721 CGGAACGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA         Db       3957 CGGAACGGGAAGGCGACTGGAGTGCCGGTTTTCAACAAACCATGCAAATGCTGA	OY 781 AIGAGGGCAICGTICCCACTGCGAIGCTGCCAACGAICAGAIGGCGCTGGGGGGAA	Qy       841       TGCGCGCCATTACCGAGTCCGGGCTTGCGTTGGTGCGGATATCTCGGTAGTGGGATACG         D       1837       TGCGGCCATTACCGAGTCCGGGCTTGGTGCGGATATCTCGGTAGTGGGATACG	OY 901 ACGATACCGAAGACACTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC	Oy         961 GCCTGCTGGGGCAAACCAGGGTGGACCGCTTGCTGCAACCTCTCTCAGGGCCAGGCGGTGA           D         3717 GCCTGCTGGGGCAAACCAGCGTGGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA	1021 AGGGGAATCAGGTGTTGCCCGTCTCACTGGTGAAAGAAAAACCACCCTGGGGGCCCAA 	1081 CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT	1141 CCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA	1201 GCAC 1204      3477 GCAC 3474	SULT 14 09-736-457-785/c	; Sequence 785, Application US/09736457 ; Patent No. 6509448 ; GENERAL INFORMATION: ; APPLICANT: Wang, Tongtong	APPLICANT: Bangur, Chaitanya S. APPLICANT: Lodes, Michael A. APPLICANT: Fanger, Gary APPLICANT: Vedvick, Tom	APPLICANT: Carter, Darrick APPLICANT: Retter, Marc APPLICANT: Mannion, Jane APPLICANT: Fan, Liqun	APPLICANT: Wang, Aijun TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

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US-09-614-124B-785/c

Sequence 785, Application US/09614124B

PARENT NO. 6630574

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Lodes, Michael A.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Marc
APPLICANT: Carter, Marc
APPLICANT: Carter, Marc
APPLICANT: Retter, Marc
APPLICANT: Netter, Marc
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C9
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FaetSEQ for Windows Version 3.0
SEQ ID NO 785
LENGTH: 5502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
36.3%; Score 1199.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1201; Conservative 0; Mismatches
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; ORGANISM: Homo sapien
US-09-614-124B-785
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Ad173609 Plasmid p
Ad173601 Plasmid p
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Ad239319 Nucleotid
Ab223939 Nucleotid
Ab32377 Tn7 door
Aa432977 Tn7 door
Ad46059 Transpose
Ad172229 DNA seque
Ad18668 Plasmid p
Ad413662 Plasmid p
Ad473099 MBP and z
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Ad033532 Vector pG
Ad033531 Vector pG
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| transl except= (pos:323..3225, as:Ha) |
| transl except= (pos:323..3225, as:Ser) |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zinc finger protein; ZFP; gene expression; modulation; plant technology; agriculture;
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                          ADL18670
ADH73599
ADH73598
ADH73600
ADH73601
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                GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Result Š.

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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant bells with a zinc finger protein (ZFP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression of the target gene in the plant for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and assircultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-mi and ZFPmi DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the
  /*tag= b
//bound_moiety= "F1-f2 primer"
2770. 2850
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                               3241 ACCGGTAAAAAACTAGTGGCCAGGCCGGCCAGTACCGCGTACGAGGTTCCGGACTACGCT 3300
                                                                                                              Zinc finger protein; ZFP; gene expression; metabolic pathway regulator; modulation; plant technology; agriculture; ds.
CCAGAATGTGGCAAGTCTTTCTCTCGGTCTGACAATCTCGTCCGGCACCAACGTACTCAC
       3181 CCAGAATGTGGCAAGTCTTTCTCTCGGTCTGACAATCTCGTCCGGCACCAACGTACTCAC
                       3241 ACCGGTAAAAAACTAGTGGCCAGGCCGGCCAGTACCGGTACGACGTTCCGGACTACGCT
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not include start and stop codon"
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bound moiety= "F1-f1 primer"
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/bound moiety= "F6-b1 primer"
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3168. 3225
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2719. .3270
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/product= "ZFPm2 prot
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                                                               AAD11589 standard; DNA; 3300
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target nucleotide sequence, where the expression of the target gene in the plant culls is modulating or regulating gene expression of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the patrial sequence of pMal-m2 and ZFPm2 DNA
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1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60
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2941 AAGTCTTTCTCTCGGTCTGACAATCTCGTCGGCACCAACGTACTCACACCGGGGGGGAGAAG 3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCAGCCGCAGCGATAACCTGGTGCGCCAC 3060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3001 CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCAGCCGCAGGGATAACCTGGTGCGCCAC 3060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3061 CAGCGTACCCACACGGGTGAAAACCGTATAATGCCCAGAGTGCGGCAAATCTTTTAGC 3120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGAATGTGGCAAGTCTTTCTCTCGGTCTGACAATCTCGTCCGGCACCAACGTACTCAC 3240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              finger protein; ZFP; gene expression; metabolic pathway regulator; lation; plant technology; agriculture; Ap3; APETALA3; ds.
                                                                                    CCGGAATGTGGTAAGTCCTTCTCTCAGAGCTCTCACCTGGTGCGCCACCAGGGTACCCAC
                                                                                                                                            ccedalaterecratectriciteresascriciterecracese
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//cransl_except = (pos:3127. 3129, aa:Ser)
//cransl_except = (pos:3136. 3138, aa:Val)
//cransl_except = (pos:3136. 3138, aa:Val)
//ortes = "CDS does not include start and stop codon"
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/bound_moiety= "F1-f1 primer"
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/bound_moiety= "F1-f2 primer"
2770. .2850
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2719. .3270
/*tag= a
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2740. .27
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) Which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-Ap3 (APETALA3) and ZFPAp3 DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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/bound_moiety= "F4-f2 primer"
3022. _3102
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                                                                                primer"
                                                                                                                                                                                                                                                                                                         "F4-f1 primer"
                                                                                                                                                        primer'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "F6-bl primer"
_moiety= "F2-f primer"
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Pred. No. 0;
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                                                                        /bound_moiety= "F3-b1
2953. .3021
                                                                                                                                                        "F3-b2
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC.
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21-JUL-2000; 2000US-00620897.
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98.6%;
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Best Local Similarity 98.64
Matches 3254; Conservative
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1081 CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT 1 1141 CCCGACTGGAAAGCGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA	1141 CCGARTIGGARAGCGGGCGCACCACACACATTAATGTGAGTTAGCTCACTCA	1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1	1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTGCGCCGACATCATAACGGTT 1	1381 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGG 1 	1441 ATTGTGAGGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1 	1501 GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG 1 		1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1 	1681 GCGCDACTGGCGATGGCCCTGACATTATCTTCTGGGCACGCCGCTTTGGTGGCTAC 1	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTT 1	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1 		1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCTGAGGGGGTTATGCGTTCAAG ;	2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG ; [	2101 GGTCTGGCTTCCTGGTTGACCTGATTAAAACAAACAATGCAGACACGATTAC 2 	2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCCTGG 2 
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	GTCAATTCAGGGTGGTGATGTGAAACCAGTAATACGATGTCGCAGAGTATGCCG 1 GTGTCTTATCAGACGTTTCCCGCGTGGTGAACCAGCCAGC	121 GTGTCTTTTTCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGGCACGTTTCTGCGAAAA 180  181 GGCGGGAAAAAAGTGGAAGCGGCGATGGCGGACCTGAATTACATTCCCAACCGCGTGCAC 240  181 CGCGGAAAAAGTTGAAAGTGCAATGCGAAACTGAACTTACAATTCCCAACCGCGTGCAA 240  181 CGCGGAAAAAAGTGAAAGTGAAAGTGAAACTGAAACTGAAAAAAAA	ACCACTGGGGGGGCAACGGGGGGGGGGGGGGGGGGGGGG	301 ACGCGCCGTCGCAAATTGTCGCGCGATTAAATCTCGCGCCGATCAACTGGCTGCCAGCG 	361 TGGTGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGGGGGTGCAAATCAATC	TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 	481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA 540	541 CACCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGGCGTC 600 	TGGTCGCATTGGGTCACCAGCAATCGCGCTGTTAGCGGGCCCCATTAAGTTCTGTCTCGG	CGCGTCTGCGTCTGGCTGCGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG	CGGAACGCGAAGGCGACTGGAGTGCCCATGTCCGGTTTTCACAAACCATGCAAATGCTGAATGCTGAATGCTGAATGCTGAATGCTGAATGCTGAATGCTGAATGCTGAATGCTGAATGCTTTTTTTT	ATGAGGGCATCGTTCCCACTGCCATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAAACGATCACATGCCCATGCCCAACGATCAATGGCGCTTGGCCGAA		ACAGGATTTTC              ACAGGATTTTC	961 GCCTGCTGGGGCAAACCAGGGTGGACGGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 	1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACACCCC1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAAAA	1081 GGCAACCGCTCTCCCCGCGTTGGTTCATTAATGCAGCTGGCACGACAGTTTTTAATGCAGCACGACAGGTTTTTTTAATGCAGCACGACAGGTTTTTTTAATGCAGCACGACAGGTTTTTTTAATGCAGCACGACAGGTTTTTTTT
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metabolic pathway regulator;
ds.
                                                                                                                                                                                                                                      'product = "ZFPm4 protein"
'transl_except = (pos:3046. .3048, aa:Ser)
'note = "CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= g
/bound_moiety= "F3-b2 primer"
2992. 3042
/*tag= h
/bound_moiety= "F4-f2 primer"
3022. 3102
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*tag= b
bound moiety= "F1-f2 primer"
770. .2850
                                                                                                                                                                                                                                                                                                                                           *tag= c
/bound moiety= "F1-f1 primer"
2824. .2889
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| Pbound moiety= "F3-b1 primer"
| 13021
| *tag= 9
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/bound_moiety= "F6-b1 primer"
3205. .3273
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/bound_moiety= "F2-b primer"
2867. .2940
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'bound moiety= "F2-f primer"
1916. _2973
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|Dound moiety= "F5-f primer"
|3168, 3225
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                                                                                                                                   Zinc finger protein; ZFP; gene expression; modulation; plant technology; agriculture;
                                                                                                         Partial sequence of pMal-m4 and ZFPm4 DNA
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bound_moiety= "F5-b
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC.
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                              AAD11591 standard; DNA; 3300
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21-JUL-2000; 2000US-00620897.
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                                                  AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (EFP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target nucleotide sequence, where the expression of the target gene in the plant cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-m4 and ZFPPMA DNA New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of target gene. Example 4; Page 145-147; 156pp; English P-PSDB; AAE06004 

Sequence 3300 BP; 849 A; 865 C; 880 G; 706 T; 0 U; 0 Other;

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1681 GCGCCAACTGGCCGTTGACCCTGACATTATCTTCTGGGCACACGGCTTTGGTGGCTAC 1740

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target on nucleotide sequence, where the expression of the target gene in the plant cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with
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Partial sequence of pMal-m3 and ZFPm3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of target gene.
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Nucleotide sequence of human Cdc25C phosphatase DNA

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                                                                                                                                                                                                                                                                                                                                                  fusion protein of maltose-binding protein and Cdc phosphatase, useful identifying phosphatase modulators for regulating the cell cycle.
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Iltose binding protein; MBP; Cdc25C phosphatase;
Cdc25B3; cyclin-dependent kinase; CDK; cell division;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                     Ducommun B,
                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 9-13; 56pp; French
                                                                                                                                                                                      14-DEC-1999; 99FR-00015722.
30-MAY-2000; 2000FR-00006883.
21-SEP-2000; 2000FR-00012008.
                                                                                                                                                        2000WO-FR003496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.9%;
Matches 2707; Conservative
   protein; maltose
; Cdc25B2; Cdc25B
                                                                                                                                                                                                                                                                                    Goubin-Gramatica F,
                                                                                                                                                                                                                                                                                                                     WPI; 2001-398152/42
                                                              Homo sapiens.
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   Fusion pro
Cdc25B1; (
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                                                                                                                                                                                                                                                                                                                                                  Cdc2SC phosphatase, amine; Cdc2S phosphatase; spontaneous alopecia; alopecia; proliferative disease; parasitic disease; viral infection; neurodegenerative disease; myopathy; angiogenesis; psoriasis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cdc25 Phosphatase inhibiting medicaments, useful e.g. for treating tumor diseases, viral infections, neurodegenerative disease or alopecia, containing new or known aryl-substituted amines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents pMAL-Hscdc25C, a plasmid encoding human Cdc25C phosphatase. The specification describes the use of aryl-substituted secondary or tertiary amines for the production of medicaments for inhibiting Cdc25 phosphatases, especially Cdc25C phosphatases. The amines of the invention are used for treating spontaneous alopecia or alopecia induced by exogenous products or radiation. They are also used for treating tumoural or non-tumoural proliferative diseases, parastic diseases, viral infections, neurodegenerative diseases or myopathy. Examples of non-tumoural proliferative diseases are e.g. angiogenesis, psoriasis or restenosis. The amines are also useful for inhibiting the proliferation of microorganisms (especially yeasts) and in the treatment of all disorders conventionally treated with vitamin K or its derivatives
                     2641 AACAACAACAATAACAATAACAACCTCGGGATCGAGGGAAGGATTTCAGAATTC
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/note= "encodes maltose binding
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                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of pMAL-Hs Cdc25C.
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                                  ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT
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Best Local Similarity   9.34;   Secte 2705.8;   DB 6;   Length 8101;	661 CGCGTCTGGCTGGCTGGCTAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720 [
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                   TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
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                                                                       2221 GCATGGTCCAACATCGACAAGAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
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P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                         encoding MBP-ToxoP30del8(82-294aa) fusion protein.
      BP.
AD023608 standard; DNA; 7259
                                                                                 (first entry)
                                                                                                                                                                                                                                               Toxoplasma gondii
                                                                                                                                                                                                                                                                                                         US2004067239-A1.
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                                                                                                                                                                                                                                                                       Synthetic.
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MBP-Toxo3
                                          ADO23608;
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02-OCT-2002; 2002US-00263153 02-OCT-2002; 2002US-00263153

MAINE G T. PATEL C B. GINSBURG S R BLIESE T R.

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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30de12C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acid sequence in amino acid sequence of Toxo30de13C P30 antigen sequence is substituted amino acid sequence of Toxo30de13C P30 antigen sequence chosen from MBP-Toxo30de13C(52-30aa) MBP-Toxo30de14C(52-294aa) and MBP-Toxo30miX1 antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies antibody complexes. The presence sequence represence of [I] I may be antibody complexes. The presence sequence represence of (I)/IgM antibody complexes. The presence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.
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                                                                                                                                                                                                    Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del1C, Toxo30del2C, Toxo530 MIXI, useful for detecting presence of IgM or antibodies to Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 7259;
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81.5%; Score 2690.4;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches
    Bliese
Ginsburg SR,
                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Fig 22; 114pp; English
    Patel CB,
                                                                              2004-304563/28
                                                                                                                          P-PSDB; AD023609
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241 AACAACTGGGGGGGAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC 300
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      AACAACTGGCGGCCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a purified P30 antigen (1) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30del3C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence consent from MBP-Toxo30del3C(52-300aa), MBP-TOXO30del4C(52-294aa) and MBP-TOXO30MIX1 fusion proteins. (1) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (1) and detecting the presence of (1)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-TOXOP30 fusion protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCAATTCAGGGTGGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
                                                                                P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.5%; Score 2690.4; DB 12; Length 7322;
99.8%; Pred. No. 0;
tive 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7322 BP; 1887 A; 1844 C; 1934 G; 1657 T; 0 U; 0 Other;
                                         DNA encoding MBP-ToxoP30del10(52-284aa) fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bliese TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ginsburg SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 25; 114pp; English
                                                                                                                                                                                                                                                                                                                                 02-OCT-2002; 2002US-00263153
                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2002; 2002US-00263153
                                                                                                                                 Toxoplasma gondii; ds; gene.
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 99.83
Matches 2694; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    (MAIN/) MAINE G T.
(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maine GT, Patel CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-304563/28.
                                                                                                                                                                           Toxoplasma gondii
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01-JUL-2004
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The invention relates to a purified P30 antigen (1) chosen from 3 fully defined Toxo30de13C, Toxo30de12C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the with alamine, or comprising the amino acid sequence in with alamine, or comprising the amino acid sequence chosen from MBP-Toxo30de13C(52-300aa), MBP-Toxo30de14C(52-294aa) and MBP-Toxo30MIX1 fusion proteins. (1) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30de13C, Toxo30de12C, Toxo230de12C, Toxo230de12C, antibodies to Toxoplasma gondii.
                                                        ††GGCGAAAGA†CCACGTATTGCCGCCACTATGGAAAAGGCCCAGAAAAGGTGAAATCATG
                                                                                                                                                                                                     GCCAGCGGTCATCACACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG
 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
                                                                                                                                           ccgaacarcccccagarcrcccrrrcrcgrarcccrccaacarcaccarc
                                                                                                                                                                                                                                                                         TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG
                                                                                                             CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
                                                                                                                                                                                GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG
                                                                                                                                                                                                                                                      P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding MBP-ToxoP30del4C(52-294aa) fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 19; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MAIN/) MAINE G T.
(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maine GT, Patel CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-304563/28.
                                                                                                                                                                                                                                                                                                                                                                                    ADO23603 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxoplasma gondii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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                                                                         CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA
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GCACTTCACCAACAAGGACCATAGCATATGAAAATCGAAGAAGGTAAACTGGTAATCTGG
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8883	with a composition comprising (I) and detecting the presence of (I)/ $IgM$ antibody complexes. The present sequence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.	δ	961 GCCTGCT(
\$ 8°	Sequence 7352 BP; 1896 A; 1852 C; 1943 G; 1661 T; 0 U; 0 Other;	අු ,	
288	Query Match Best Local Similarity 99.8%; Pred. No. 0; Matches 2694; Conservative 0: Mismatches 6: Indels 0: Gans 0.	Š 8	1021 AGGCCAN 
ò	SCADARCCTTTCGCGGTATGGGCTGATAGCGCCCGGAAGAGA 60	oy d	1081 CGCAAAC
යු	1 ccacaccatcaaatgorecaaaaccrrrcgcdgrafdccatgaragcgcccggaagag 60	a à	1141 CCGBCTC
දි සි	61 GTCAATTCAGGGTGGTAAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120 	qo	
ò		ò	1201 GCACAAT
q	121 GIGICTCTTATCAGACCGTTTCCCGCGTGGACCAGGCCAGCCACGTTTCTGCGAAAA 180	ପ୍ର ପ୍ର	
දි සි	181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240	<b>3</b> 8	1261 TCAGGCAC         1261 TCAGGCAC
ò	241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCACCTCGCCTGC 300	à	1321 TGTCGCTC
qq	241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCACTCGCCCTGCC300	qu	1321 TGTCGCTC
ò	301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCCGATCAACTGGGTGCCGGGG 360	yo f	1381 CTGGCAA
셤	301 ACGCCCTCCCAAATTGTCCCCGATTAATCTCCCCGATCAACTGGGTGCCAGCC 360	3 8	1441 ATTGTGAC
કે ક	361 TGGTGGTGTGGATGGTAGGAACGAAGGGGCGTCGAAGCCTGTAAAGCGGCGGTGCAAATC 420	g qq	1441 ATTGTGAC
3 8	1661661CGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	δ	1501 GCACTTC
<b>3</b> 8	** ILLOGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	qu	  1501 GCACTTC
ò		ð i	
셤	481 TIGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTTCTGACCAGA 540	g :	
8 8	CACCCATCAACAGTATTATTTCTCCCATGAACACGGTACGCGACTGGGCGTGGAGCATC	<b>À</b> A	1621 ACCGGAT         1621 ACCGGAT
3 8	5*1 CACCCATGAGGAGGATTATTTCTCCCATGAGGAGGGGAGGGGGGGG	δ	1681 GCGGCAAC
. A	TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG	qq	1681 GCGGCAAC
ò	661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAT	රු සි	1741 GCTCAATC
ପ୍ର	661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720	3 8	1901 CCTUMAIC
ठे ह	CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA	දි දි	1801 CCGIIIAC          1801 CCGTTTAC
8 8	CUGAACCGGGAGCGACTGGGGGTTGTCCGGGTTTTCAACAAACCATGCAAATGCTGA	à	1861 GAAGCGTT
දු දු	781 ATGAGGGCATCCCACTGCGATGCTGGTTGCCGATGATGATGGGTGGG	qa	 1861 GAAGCGTT
à	TGCGCGCCATTACCGAGTCCGGGCTGCGCTTGGTGCGGATATCTCGGTAGTGGGATACG	ò	1921 GAGATCCC
đ		qa .	1921 GAGATCC
ે t	ACGATACCGAAGACAGCTCATGTTATATCCCGCGGTTAACCACCATCAACAGGATTTTC	<b>장</b> 점	1981 CTGCAAGA         1981 CTGCAAGA
£	901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 960		

à i	61 GCTGCTGGGGGAAACCAGGGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1
g 8	bi GUCTGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
λό d	1021 AGGGCATCACTGTTGCCCGTCTCACTGAAAAAAAAACAACCTGGCGCCCAATA 1080 
ò	81 CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACAGGTTTTTTAATGCAGCTGGCACAGGTTTTTAATGCAGCTTGCACAGGTTTTAATGCAGCTTGCAATGCAGCAATTTAATGCAGCTTGGCAGGTTTTAATGCAGCTTGGCAGGTTTTAATGCAGCTTGGCAGCTTGGAATTTAATGCAGCTTGGCAGGTTTTAATGCAGCTTGGCAGGTTTTAATGCAGCTTGGAATTTAATGCAGCTTGGCAGGTTTGAATTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGCTTGGAATTTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTTAATGAATTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTTAATGCAGAATTAATT
qq	81 CGCAAACCGCCTCTCCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGCGTTT
ò	rh
qq	41 CCCGACTGGAAAGCGGCAGTGAGCGCAACGCAATTAATGTAAGTTAGCTCACTCA
ò a	GCTTCTGGCG 1
ò	61 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAAGATCACTGCAAAATTCG
qq	61 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG
à	21 IGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGGCACATCATAACGGTT
qa	GCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGGACATCATAAAGGTT
ζ	CABATATICTGABATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGGA
qu	81 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA
ò	41 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA
qu	41 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA
ζ	01 GCACTTCACCAACAAGGACCATAGATATGAAAACTGAAGAAGGTAAACTGGTAATCTGG
qu	1501 GCACTTCACCAACAAGGACCATAGCATATGAAAATCGAAGAAGGTAAACTGGTAATCTGG 1560
λõ	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT 1620
qa	61 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGATTCGAGAAAGAT
<i>ك</i> ة	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAAATTCCCACAGGTT 1680
qa	21 ACCGGAATTAAAGTCACCGGTTGAGCATCCGGATAAACTGGAAGAAAAATTCCCACAGGTT
ò	81 GCGGCAACTGGCCGTTGGCCTTATCTTCTGGGCACACGACCGCTTTGGTGCCTAC
qq	1 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACGGCTTTGGTGGCTAC
ò	1 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT
අු	1741 GCTCAATCTGGCCTGTTGGCTGAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTGT 1800
ò	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATGGCTGTT 1860
q <sub>Q</sub>	  GTT 186
70	CTGCTGCCGAACCCGCCAAAAACCTGGGAA 197
qa	SOTIATION OF THE STATE OF THE S
ò	CAAC 198
qq	21 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCGC
ζō	CAAG 2
d d	GAAGAACCGTACTICACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCTTCAG 204

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                                                                                                                                                                                                                   The invention relates to a purified P30 antigen (1) chosen from 3 fully defined Toxo30de12C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30de13C P30 antigen sequence in substituted with alanine, or comprising the amino acid sequence chosen from MBP-Toxo30de13C(52-300aa), MBP-Toxo30de14C(52-29aa) and MBP-ToxO30MIX1 fusion proteins. (1) is useful for detecting the presence of IGM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IGM antibodies with a composition comprising (1) and detecting the presence of (1)/IGM antibody complexes. The present sequence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.
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                                                                                                           Novel purified polypeptide having sequence identity to amino acid sequence of F93 antigen of Toxoplasma gondii e.g. Toxo30de13C, Toxo30de12C, Toxo30de12C, Toxo910 MIXI, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
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99.8%; Pred. No. 0;
iive 0; Mismatches
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Matches 2694; Conservative
                               Patel CB,
                                                              WPI; 2004-304563/28
P-PSDB; ADO23599.
 BLIESE T R.
                                 Maine GT,
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                                 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
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AGGCCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAAACCACCCTGGCGCCCAATA 1080 CGCGTCTGCGTCTGGCTGGCTAAATATCTCACTCGCAATCAAATTCAGCCGATAG CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAAGCCGGTGA ATGAGGGCATCGTTCCCACTGCGATGCTTGCCAACGATCAGATGGCGCTGGGCGCAA CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA GCACTTCACCAACAAGAACCATAGATATGAAAACTGAAGAAGGTAAACTGGTAATCTGG ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA ATTGTGAGGGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 

  CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGGAGAAGGTAAGGTAAGTTCTAAC CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGTTATGCGTTCAAG CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGTTATGCGTTCAAG TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2401 GAAGCGGTTAATAAAGACAAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2221 GCATGGTCCAACATCGACAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGATGATGAAGGTCTG 2341 CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGCTGATGAAGGTCTG 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATGATCAACGCC TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG CCGAACATCCCGCAGATGTCCGGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAAGACGCGCAGACTAATTCGAGCTCG 8 6 \$ B \$ 엄 8 8 8 g 중 염 S 8 9 g 요 a ò ò g ò

RESULT 12 ADO23639 ID ADO23

ADO23639 standard; DNA; 7370

ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT

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                                                         AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTGC
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                                                                                                                           P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 7370;
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                                                                                          DNA encoding MBP-ToxoP30MIX1 fusion protein.
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                                                         (first entry)
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PATEL C B.
GINSBURG S R.
BLIESE T R.
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Synthetic.
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1261 TCAGGCAGCCATCGGAAGCTGTGGTATGCCTGCAGATCACTGCATAATTCG   1320   1321 TGTCGCTCAAGGCGCACTCTGCGATAATGTTTTTGCGCCGACATCATAACGGTT   1380   1321 TGTCGCTCAAGGCGCACTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT   1380   1321 TGTCGCTCAAGGCGCACTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT   1380   1381 CTGGCAAATATTCTGAAATGACTGTTGACAATTAATCATCGGCTCCTATAATGTGTGGA   1440   1441 ATTGTGAGCGATAACAATTCACAAGAAATATCACAAGAAACAATTCACAAGAAACAATTCACAAGAAACAATTCACAAGAAACAATTCACAAGAAATTCACAAGAAACAATTCACAAGAAACAATTCACAAGAAACAATTCACAAGAAACAATTCACAAGAAACAATTCACAAGAAACAATTCACAAGAAAACAATTCACAAGAAAACAATTCACAAGAAAAAACAATTCACAAGAAAACAATTCACAAGAAAACAATTCACAAGAAAACAATTCACAAGAAACAATTCACAAGAAAAAAATTTCACAAGAAAAAAAA		1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680  1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680  1681 GCGGCAACTGGCGATGACGCTTGAGCATCCTGGGCACACGCTTTGGTGGCTAC 1740  1681 GCGGCAACTGGCGATGGCCTGACATTATCTTCTGGGCACGCTTTGGTGGCTAC 1740  1681 GCGGCAACTGGCCGTTGACATTATCTTCTGGGCACGCTTTGGTGGCTAC 1740	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGGGTTCCAGGACAAGCTTAT 1800  1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGGGTTCCAGGACAAGCTGTAT 1800  1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAGAAGTGGTTACCCGATGGCTGTT 1860  1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGTGTTACCTGCTGTT 1860  1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATGGTTT 1860	1861   GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGGCCAAAACCTGGGAA 1920	1981   CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCGGGGGTTATGCGTTCAAG 2040   1981   CTGCAAGAACCGTACTTCACCTGGCGCTGATTGCTGCTGCGGGGGTTATGCGTTCAAG 2040   1981   CTGCAAGAACCGTACTTGACTGGTGATTGCTGCTGCGGGGGGTTATGCGTTCAAG 2040   2041 TATGAAAACGGCAAGTATAAAAGACGTTGAGGGGTGGATAAACGCTGGGGGGGAAAGCG 2100   1	2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACAATGAATG	2221 GGATGGTCCAACATCGACAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280 2221 GCATGGTCCAACATCGACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280 2221 GCATGGTCCAACCGTCGACACCCAGCAAATTATGGGTGAACGGTACTAACGCCGACCTTC 2280 2281 AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT 2340 2281 AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT 2340 2341 CCGAACAAAGAGCTGGCAAAAAGATTCCTCGAAAACTATCTGCTGATGAAGGTCTG 2400 2341 CCGAACAAAAGAGTTCCTCGAAAACTATCTGCTGATGAAGGTCTG 2400 2341 CCGAACAAAAGAGTTCCTCGAAAACTATCTGCTGATGAAGGTCTG 2400

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antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-Toxop30 fusion protein of the invention.
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Patel CB,

PATEL C B. GINSBURG S R. BLIESE T R.

us-09-765-555b-15.rng

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Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo50del2C, Toxop30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
                                                                                                                         Example 5; Fig 33; 114pp; English.
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P-PSDB; ADO23645.
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding MBP-ToxoP30MIX3 fusion protein.
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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30de13C, Toxo30de12C and Toxo330 MTX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30de13C P30 antigen sequence is substituted with alamine, or comprising the amino acid sequence chosen from MBP-CT Toxo30de13C(52-30daa), MBP-Toxo30de14C(52-294aa) and matabodies antibodies to Toxo30de14C(50) antibody complexes. The present sequence represents DNA encoding a MBP-Toxo930 fusion protein of the invention.
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                                                                                                                                                                                   P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
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P-PSDB; ADO23595.
                       ADO23594 standard;
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AKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATWENAQKGEIMPNI POWASHWYAVRTAVINAASGGTVDEALKDAGTUNSSNINNINNINLIGIEGRISEFG SSSPGKPPRLVGGPWDASVEEEGVRAALDFAVGEYNKASNIDMYHSRALOVVRARKQIV AGVNYPLDVELGRTTCTKTQPNLDNCPHDQPHLKRKARCSFQTYAVPWQCTMTLSKS TCQDAASASHHHHHHHHARETAQAKHKQRKRLKSSCKRHPLYVDFSDVGWNDWIVAPPCYH AFYGHGECPPPLADHLMSTNHAIVQTLVNSVNSKIPKACCVPTELSAISMLYLDENEK VVLKNYQDMVVBGCGCR" wisc_feature ACIDSEquenz)" ACIDSECUENZ ACIDSEQUENZ AC	Query Match         82.0%;         Score 2705.8;         DB 6;         Length 7373;           Best Local Similarity         99.2%;         Pred. No. 0;           Matches 2719;         Conservative         0;         Mismatches         22;         Indels         0;         Gaps         0;           Qy         1         CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATGATGGCCCGGAAGAGA         60         1   1	61 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG	CGCGGGGAAAAGTGGAAGCGGGGATGGCGGAGCGGGGGGGAACGGGGGAAAGTGGAAGCGGGGGGATGGCGGGGGGGG		Qy         481         TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA 540           Db         481         TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATCTTCACCAGA 540           Qy         541         CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGGGCTGGAGCATC 600           Db         541         CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGGGCTGGAGCATC 600           OV         601         TGGTCGCATTGACTCACCAAAAAAAAGACGGTACGGACTGGGCGTGGAGCATC 600	601 661 661 721 721 781
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          FEATURES
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	RESULT 12 AX377532 LOCUS DEFINITION Sequence 9 from Patent W00212553. VERSION AX377532 01:19573718 KEYWORS SOURCE Synthetic construct ORGANISM Synthetic construct	NCE ORS B NAL NAL	Query Match         81.8%;         Score 2698;         DB 6;         Length 9191;           Best Local Similarity         99.8%;         Pred. No. 0;         Anatches 2701;         Conservative         0;         Mismatches 5;         Indels 0;         Gaps 0;           Qy         1         CCGACACCATCGAAATGCTGCAAAACCTTTCGCGGTATGGCATGATAGGCCCGGAAGAG 60	Qy         61 GTCAATTCAGGGTGGTGAAACCTGAAACCGTTATACGATGTCGCAGGTATGCCG         120           Db         61 GTCAATTCAGGGTGGTGAATGTGAAACCATAACGATGTCGCAGGTTTGCCG         120           Qy         121 GTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGGCTTTCTGCGAAA         180           Db         121 GTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGCTTTCTGCGAAA         180	Qy         181 CGCGGGAAAAAGTGGAAGCGCGATGGCGGGGCTGAATTACATTCCCAACCGCGTGGCAC 240           Db         181 CGCGGGAAAAAAGTGGAAGCGGCGATGGCGGACTGAATTACATTCCCAACCGCGTGGCAC 240           Qy         241 AACAACTGGCGGGCGAACGTTGCTGATTGCCACCTCCACTCTGGCCTGC 300           Db         241 AACAACTGGCGGCAACAGTCGTTGCTGATTGCCACCTCCAGTCTGGCCTTGC 300	Oy         301 ACGCGCCGTCGCCAATTGTCGCGCCATTAAATCTCGCGCCCATCAACTGGGTGCCAGCG         360           Db         301 ACGCGCGTCGCAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG         360           Oy         361 TGGTGGTGCGTGGAACGAACGAGCGGCTCGAAGCCTGTAAAGCGGGGTGCAAATC         420           Db         361 TGGTGGTTCGATGGTAACGAACGACGGCTCGAAGCCTGTAAAAGCGGGGTGCAAATC         420	421 TTGCGGGAAGGGTGATCATTAACTATCGGTGGATGACCAGGAGCAGCATTAACTATCGGTGGATGACCAGGATGCCATTAACTATCGGTGGATGACCAGGATGCCATTAACTATCGGTGGATGACCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGCCAGGATGAGATGCTAATGTTCCGGCGTTATTTCTTGATGTCCTCAGCCAGATGATGTTAATTTTCTTGATGTCTCTGACGAGAAGCTGCCAGAAGCTGCCCATGATGTTCCCAGGAGGCTGGCGGACCGGAGAAGCTGCCCATGAAGGATCTCTCAGAGGCATCCCATGAAGGCTGGGCGTGGAGCGTCCCATGAAGCTATTTTTTTT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 6724)
Sheffield, P.J., Garrard, S.M. and Derewenda, Z.S.
Direct Submission
Submission
Submitted (05-007-1998) Molecular Physiology and Biological
Physics, University of Virginia, 4215 Jordan Hall, 1300 Jefferson
Park Avenue, Charlottesville, Virginia 22908, USA
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M Expression vector pMBP-parallell
other sequences; artificial sequences; vectors.

1 (bases 1 to 6724)
Sheffield, P., Garrard, S. and Derewenda, Z.
Overcoming expression and purification problems of family of 'parallel' expression vectors
Protein Expr. Purif. 15 (1), 34-39 (1999)
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/note="multiple c. 3426. 4356

/gene="bla"

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1981   CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCTGGCGGGTTATGCGTTCAAG 2040	RESULT 15 AF031088 LOCUS LOCUS Shuttle vector pMAL-pIII, complete sequence. ACCESSION AF031088
10.1   TGCGCCCCATTACCGAGTCGGGGTGGCGGTGGCGGATATCTCGGTAGTGGGATTAC   900   901   ACGATACCGAAGACAGGGTTATATCCCGCCGGTTAACCACACACA	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAATTCGAGAAAGAT   1620

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                                                              Score 2631; DB; Pred. No. 0; Mismatches
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NNNNNNNNNLGIEGEIRPNIGOMSAFWAGGGG"
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'Gene="malE-lacZa fusion"
/product="malE-lacZa fusion"
fusion protein"
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[New England Biolabs]"
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note="M13 secretion signal sequence"
                                                                                                                                                                                                                                             note="transcriptional repressor"
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xref="taxon:69327"
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                                                                                                                                                                      gene="lacI"
                                                                                                                                                                                              i. .1163
gene="laci"
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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: August 2, 2005, 10:29:49; Search time 6743.2 Seconds

(without alignments)

18627.964 Million cell updates/sec

18627.964 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088
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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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CB862524 AL048427 AL042909 CA881974 CA890032 CA890032 CA890032 AL039076 AL039076 AL039128 AL039589 CA8863409	ALIGNMENTS 794 bp totrichum trif	341 1ii 1ii comycota; rrae sedis raceae; CoJ	M., Town, C.C.M. Colletotri 8 Samac Samac Pathology	91 Upper Bu i.crl.umn.e MTSAH67TV P CGA CtC AG	colletotrii mRNA" mRNA" axon:5466" c="mycelia" "Young, acia" "Young, acia" "Young, cer "Young, cer "Young, cer "Young, cer "Young, acia" "Sglucese) "DH5allues "DSCT" "DSCT" "The cDNA and packag
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E. coli Y1090 and phage DNA was purified from a liquid lysate. The CDNA inserts were gel purified after ECORI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DHSalpha which were plated onto medium with X-gal for selection of recombinants."
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                                                                                                                                                                              Length 794;
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                                                                                                                                                                       Score 778; DB 5; I
Pred. No. 4.9e-219;
0; Mismatches 10;
                                                                                                                                                                     23.6%;
Local Similarity 98.7%;
Nes 784; Conservative 0
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CK394523 779 bp mRNA linear EST 30-DEC-2003 hggada4D08 Gland Cell Amplified cDNA Library Heterodera glycines

CK394523/c LOCUS DEFINITION

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Heterodera glycines

Heterodera glycines

Heterodera glycines

Heterodera glycines

Heterodera glycines

Eukaryota; Medazoa; Nematoda, Chromadorea; Tylenchida; Tylenchida;

Tylenchoidea; Heteroderidae; Heterodera.

I (bases 1 to 779)

S Wang, X., Allen, R., Gao, B., Goellner, M., Maier, T., Baum, T.,

Hussey, R. and Davis, B.

Submission: Wang, Allen, Gao, Goellner, Maier, Baum, Hussey, Davis

Longublished (2003)

Contact: Tom Maier

Department of Plant Pathology, Baum Lab

Jowa State University

JSI Bessey Hall, Ames, IA 50011, USA

Tel: 515-294-8854
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/organism="Heterodera glycines"

/organism="RNA"

/db_xref="teaxon:51029"

/cell type="gland"

/dev_frage="mixed parasitic juvenile"

/dev_frage="mixed parasitic juvenile"

/cone lib="gland cell Amplified cDNA Library"

/note="Organ: gland cell; Vector: pSportII"
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Pred. No. 7.6e-217;
0; Mismatches 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: trmaier@iastate.edu
Heterodera glycines Gland (
CK394523
CK394523.1 GI:40389794
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Best Local Similarity 99.4%;
Matches 773; Conservative C
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RESULT 3 CK118014 LOCUS DEFINITION

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ACCESSION

REFERENCE AUTHORS TITLE

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985 ACCGCTTGCTGCAACTCTCTCAGGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCT 1044
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EST632218 DSCT Colletotrichum trifolii cDNA clone pDSCT6-59, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collectrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 793)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 ATABATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGT
                                                                                                                                                                                                   361 CCATGTCCGGTTTTCAACAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 CCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAA
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                                                          385 GCGCCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGC
                                                                                       GCGCCTCGAAGCCTGTAAAGCGCCGTGCACAATCTTCTCGCGCCAACGCGTCAGTGGCC
                                                                                                                                                                   TGATCATTAACTATCCGCTGGATGACCAGGATGCCATTGCTGTGGAAGCTGCCTCCACTA
                                                                                                                                                                                                                                                                            ATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTTCT
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  Gaps
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Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,
Cheung,F. and Fraser,C.M.
ESTs from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
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  768; Conservative
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5-PRIME, mRNA sequence.
CK118014
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bokematophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 76)
Feilner,T., Immink,R.G.H., Cahill,D.J. and Kersten,B.
Generation of a cDNA expression library from Arabidopsis
inflorescence meristem
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Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Ihnestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131128
Email: Kersten@molgen.mpg.de
Insert Length: 769 Std Brror: 0.00
Plate: 218 row: N column: 6
Seq primer: p0E65.
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/organism="Arabidopsis thaliana"
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/ecoType="Columbia"
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clone="MPMGp2011N06218"
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/dev stage="Young, actively growing mycelia (3 days after inculation) grown in liquid culture (cutin minimal medium containing 2%ducose)."
/lab_host="DHSalpha"
/clone_lib="DSCT"
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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mitosporic Phyllachoraceae; Colletotrichum,
                 GCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA
                                                                                        CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTG
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Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T., Cheung, F. and Fraser, C.M.
ESTS from mycella of Colletotrichum trifolii race 1
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Other ESTS: EST611782
Contact: Deborah A. Samac
Departshy of Minnesota
195 Borlaug Hall, 1991 Upper Buford Circle, St. Pau
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIRR sequence name: WTSAC64TV More information is 8
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/mol type="mRNA"
/strain="race 1"
/db xref="taxon:5466"
/clone="pDSCT3-64"
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Seq primer: (gtA AtA CgA CtC ACt AtA ggg C)
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//oote="Vector: pBluescript SK+; Site_l: ECORI; Site_2:
RCORI; isolate: 2sp2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtll from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
lyaate. The cDNA inserts were gel purified after ECORI
digestion and ligated into pBluescript SK+, Aliquots of
the ligation were used to transform E. coli DHSalpha which
were plated onto medium with X-gal for selection of
                                                                                     MN 55108, USA
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/dev stage="Young, actively growing mycelia (3 days after
incollation) grown in liquid culture (cutin minimal medium
containing 2*glucose)."
/lab_host="DH5alpha"
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             Contact: Deborah A. Samac
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbyspuccini.crl.umn.edu
TIGR sequence name: MTSAF59TV More information is availab
www.medicago.org
Seq primer: (qtA AtA CgA CtC ACt AtA ggg C).
Location/Qualifiers
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                                                                                                                                                                                                                                             /organism="Colletotrichum trifolii"
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lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DHSalpha which were plated onto medium with X-gal for selection of recombinants."
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                                                                                                                                                                      CAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGT 120
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                                                                                                                             CGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACAA
                                                                                                                                                                                                                                                                                        CAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCAC
                                                                                                                                                                                                                                                                                                  GTGGTGTCGATGGTAGAACCAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTT
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                                                                                                                                                           CAATTCAGGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGT
                                                                                                                                                                                                     CGGGAAAAAGTGGAGGGGGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTG
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                                                                                                                  GACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGT
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                                                                           Length 806;
                                                                                              Indels
                                                                        22.9%; Score 755.4; DB 5; 97.4%; Pred. No. 2.5e-212; tive 0; Mismatches 16;
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                                                                                              Conservative
                                                                                   Similarity
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CB863541 689 bp mRNA linear EST 22-APR-2003 HH04A08y HH Hordeum vulgare CDNA clone HH04A08 3-PRIME, mRNA sequence.

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                                                                                    Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 689)
Varshney, R.K., Zhang, H., Burton, R., Stein, N., Langridge, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=_Vector: pSPORT; Site 1: SalI (5-end of cDNA); Site 2: NotI (3-end of cDNA); Due to the cloning system used blue/white selection for recombinants is not 100 reliable. Average insert size is 1.3 kb."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCCCGCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTGGAAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                       Contact: Stein Nis
Molecular Markers Group, Department Genbank
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 689 Std Brror: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="coleoptile"
/dev_stage="coleoptile, 1 day old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.8%; Score 684.8; DB 6; 99.6%; Pred. No. 2.3e-191;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. 689
/organism="Hordeum vulgare"
/mol_type="mRNA"
/culfivar="Sloop"
/db_xref="GABI:55198"
/db_xref="taxon:4513"
/clone="HH04A08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                            Barley ESTs from coleoptile tissue
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                 Hordeum vulgare
Eukaryota, Viridiplantae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone lib="HH"
GI:30058100
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                                             Hordeum vulgare
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GSS 06-NOV-2002
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       552 ACGTTATACGATGTCGCAGAGTATGCCGGTGTCTTTATCAGACCGTTTCCCGCGTGGTG 593
                                                                                                                                                                                                       331 AATCTCGCCCCGATCAACTGGGTGCCAGCGTGGTGGTGGTCGATGGTAGAACGAAGCGGCG 390
                                                                                                                                                                                                                                                                             TCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATCA 450
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1 (bases 1 to 710)

Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Meda, D., Azam, F. and Rohwer, F.
Genomic analysis of uncultured marine viral communities
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AY080106 AY10 bp DNA linear GSS 06-NOV-20 AY080106 Scripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3G6L, genomic survey
                                                                                                              212 GCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTGAT
                                        AACCAGGCCAGGCACGTTTCTGCGAAAACGCGGG-AAAAAGTGGAAGCGGCGATGGCGGA
                                                                           592 AACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTGGAAGCGGCGATGGCGGA
                                                                                                                                                                              272 TGGCGTTGCCACTCCAGTCTGGCCCTGGAC-GCGCCGTCGCAAATTGTCGCGGGGGATTA
                                                                                                                                                                                                                                                                                                                                                                                                                          571 AAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biology Dept.
San Diego State University
5500 Campanile Dr, San Diego, CA 92102,
Tel: 6195941336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 619595676
Email: forest@sunstroke.sdsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                   AL038548
DKPZp566E0346_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKRZp56E0346_5', mRNA sequence.
                    560
                                                                                                        150
                                                                                                                                     TTCTCCCATGAAGACGGTACGCGACTGGCGTGGAGCATCTGGTCGCATTGGGTCACCAG 620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email 8. Wiemann@dkfz-heidelberg.de; sequenced by MediGenomix (Martinsried/Germany) within the cDNA sequencing consortium of the German Genome Project. No 81 sequence available.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACGITATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACCGTTTCCCGCGTGGTG 152
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 712)
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                                                                                      209 ACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCATCAACAGTATTATT
                                                                                                                                                             TTCTCCCATGATGATGGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone (DKFZp566E0346) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                          89 CAPATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCGTCTGGCTTGGCTTGGC
ACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 GGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAAACCAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organisms"Homo sapiens"
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/clone_lib="566 (synonym: hfkd2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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99.6%; Pred. No. 7.2e-189;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                               681 TGGCATAAATATCTCACTCGCAATCAAAT 709
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Unpublished (1999)
Contact: MIPS
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Matches 699; Conservat
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AL038548/c
LOCUS
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KEYWORDS
SOURCE
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AUTHORS
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DKFZp434I102_s1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434I102_3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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                                                                                                                                                EST (Ansorge, Benes, et al.)
Unpublished (1999)
Contact: MIPS
                                       AL044483.1 GI:5432701
EST.
                                                                                                                                                                                                                                                                                 German Genome Project
                                                                 Homo sapiens (human)
                                                                                                                 (bases 1 to 660)
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                                                                              Homo sapiens
                                                                                                                                          Wiemann, S
                             AL044483
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Best Local S
Matches 659
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                                                                 surface seawater using a combination of differential filtration and density-dependent gradient centrifugation. Linker-amplified shotgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating dsDNA linkers to the ends, and amplifying the fragments using Vent DNA polymerase. The resulting fragments were ligated into the pSMART vector and electroporated into MC12 cells (Lucigen; Middleton, WI)"
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                                                                                                                                                                                                                                                                                            67
                                                               /note="Marine viruses were isolated from 200 liters of
                                                                                                                                                                                                                                                                                                                                CGCGACTGGGCGTGGCATCTGGTCGCATTGGGTCACCACCAAATCGCGCTGTTAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCAATCAAATTCAGCCGATAGCGGAAACGGGAACTGGACTGGAGTGCCATGTCCGGTTTC
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Pred. No. 9.5e-189;
0; Mismatches 7;
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98.9%;
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Best Local Similarity 98.9
Matches 690; Conservative
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mRNA

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AL044483

ä 144 541 601 204 264 481 324 421 384 361 444 301 504 241 564 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKEZ): Email s.wiemann@dkfz-heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the and No Tiles of the RZPD is available at the RZPD in Berlin. This clone (DKFZp4341102) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de. 360 GCGGCGTCGAAGCCCTGTAAAGCGGCGGTGCAATCTTCTCGCGCAACGGGTCAGTGGGC GCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTGGAAAGCGGCGA 600 GCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAAACGCGGGAAAAAGTGGAAGCGGGA 540 TGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAAACAACTGGCGGGGCAAACAACGGT TGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCCCCTCGCAAATTGTCGCGG CGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGCTAGATGGTAGAACGAA 420 CGATTAAATCTCGCGCCGGTCAACTGGGTGCCAGCGTGGTGGTGGTGGTAGAACGAA 505 ATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTTTCT AACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACCGTTTCCC TGGCGGGAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGT GCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGC Gaps /dev\_stage="adult" /lab\_host="DH10B" /clone\_lib="434 (synonym: htes3)" /note="Vector: pSport1; Site\_1: Not1; Site\_2: Sal1" Ansorge, W., Benes, V., Krieger, S., Mewes, H.W., Gassenhuber, J. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1; Length 660; Indels tch 19.6%; Score 647.4; DB 1; al Similarity 99.7%; Pred. No. 2.9e-180; 659; Conservative 0; Mismatches 1; g ઠે

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CB863814 62-APR-2003
HH07B20y HH Hordeum vulgare cDNA clone HH07B20 3-PRIME, mRNA
sequence.
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          282
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 624)
Varshney, R.K., Zhang, H., Burton, R., Stein, N., Langridge, P. and
                                                               GAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTG
                                                                                            GAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGGAAACAGTCGTTGCTG
                                                                                                                                270 ATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCGCCGTCGCAAATTGTCGCGGCGATT
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Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
CorrensEtr. 3, 06466, Gatersleben, Germany
Tel: 039482-5595
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 624 Std Error: 0.00
Plate: 7 row: B column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   630 CIGITAGCGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCG 670
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/organism="Hordeum vulgare"
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/cultivar="Glop"
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/tissue_type="coleoptile"
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Unpublished (2003)
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1 (Dages 1 to 641)

Yitanama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
CCCATGAAGACGGTACGCGACTGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAA
                                                                                                                     CGCGGTATGGCATGATAGCGCCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAAACCA
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100.0%; Pred. No. 2.3e-178;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
11-81-81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
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/ Organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="textor:8355"
/clone="XL077k02"
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Location/Qualifiers
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BJ063872.1 GI:17471074
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This is the 3' sequence of the clone insert

Clone from 5. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); sequenced by Qiagen within the cDNA

sequencing consortium of the German Genome Project. rl sequence
also available.

This clone is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

Location/Qualifiers

1. 794
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                                                                                                                                                                                                                                                                                                                                    /tissue_type="testis"
/dev stage="adult"
/lab_host="bH108"
/clone lib="414 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
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/db_xref="taxon:9606"
/clone="DKFZp434B075"
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 EST (Duesterhoeft,
Unpublished (1999)
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Matches 634; Conservative
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Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
/dev_stage="coleoptile, 1 day old"
/lab.host="DH10B"
/clone_lib="HH"
/note="Vector: pSPORT; Site_1: SalI (5-end of cDNA);
Site_2: NorI (3-end of cDNA); Due to the cloning system used blue-white selection for recombinants is not 100 % reliable. Average insert size is 1.3 kb."
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0
                                                                                                                                                          18.7%; Score 615.8; DB 6; Length 624; ilarity 99.7%; Pred. No. 7e-171; Conservative 0; Mismatches 2; Indels 0.
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                          332 AGGCCAACCGTIGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAAGGTGGCGAAAGATC 273
                                                                                                                  212 AGAIGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATGACGCCGCCAGCGGTCGTC 153
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John Service seawater using a combination of differential filtration and density-dependent gradient centrifugation. Linker-amplified shotgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating daDNA linkers to the ends, and amplifying the fragments using Vent DNA polymerase. The resulting fragments using Vent DNA polymerase. The resulting fragments were ligated into the pSWART vector and electroporated into MC12 cells (Lucigen; Middleton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; environmental samples.

1 (bases 1 to 608)
Breitbart,M., Salamon,P., Andresen,B., Mahaffy,J.M., Segall,A.M.,
Mead,D., Azam,F. and Rohwer,F.
Genomic analysis of uncultured marine viral communities
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Scripps Pier (La Jolla, CA) uncultured virus
                                                                                                                                                                                                                                                                                                                                                                                                                              AY080094
AY080094 Scripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3D4L, genomic survey
                                                                                     CACGTATTGCCGCCACCATGGAAAACGCCCAGAAAAGGTGAAATCATGCCGAACATCCCGC
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/organism="uncultured marine virus"
/mol_type="tgenomic DNA"
/db Aref="taxon:186617"
/clone="81051p3D41"
                                                                                                                                                                                                                                                                 2594 AGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT 2628
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                                                                                                                                                                                                                                                                                                AGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Rohwer F
Biology Dept.
San Diego State University
5500 Campanile Dr, San Diego, CA 92102,
Tel: 6195941336
Fax: 619595676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: forest@sunstroke.sdsu.edu
Class: shotgun.
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                            PRIO124a_CO1 - PRIO124a.B21 (752) Mixed stage fosmid library of P. Dacificus var. California Pristionchus pacificus genomic, genomic CL655575
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1 (Dases 1 to 752)
Srinivasan, T., Otto, G. M., Kahlow, U., Geisler, R. and Sommer, R.J. Appabs an Aceds database for the nematode satellite organism Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mixed stage fosmid library of P. pacificus var. California"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39. Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf. sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Class: fosmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .752
Organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:54126"
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Pristionchus pacificus
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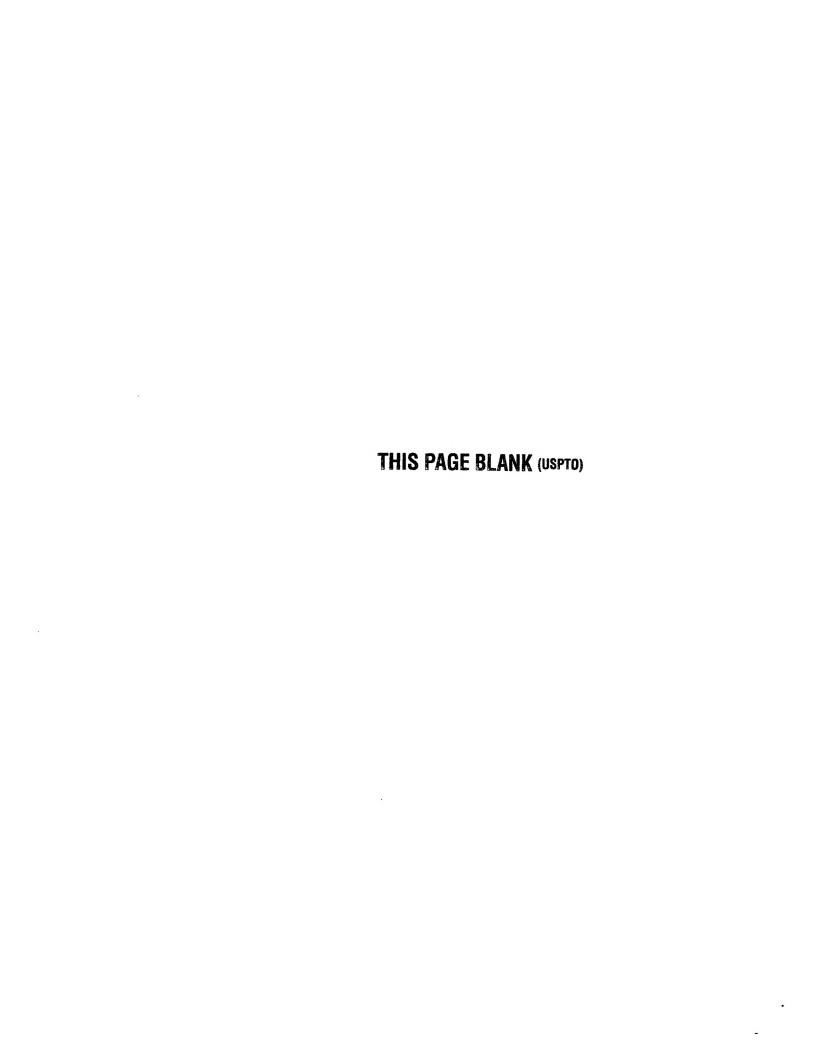
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DKFZp564C157_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
AL037742
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1 (bases 1 to 589)
Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Ltd Braunschweig/Germany) within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No all sequence available.
This clone (DKFZP564CL57) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
AAGTICTGTCTCGGCGCGTCTGCGTCTGGCTGGCTGGCTAAAATATCTCACTCGCAATCA
                                                               TGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACT
                                                                                                                                                                                                          GGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATCGCGGCTGTTAGCGGGCCCATT
                                                                                                                                                                                                                         GGGCGTGGAGCATCTGGTTGGGTCACCACCAAATCGCGCTGTTAGCGGGCCCATT
                                                                                                                                                                                                                                                              AAGTICTGGCGCGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCA
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                                                                                                    TGACCAGGATGCCATTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                        879
                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
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Unpublished (1999)
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VERSION
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/dev stage="fetal"
/lab_host="14-2blue"
/clone lib="564 (synonym: hfbr2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: Sall"
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Pred. No. 3.7e-162;
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Sequence 30, Appl Sequence 25, Appl Sequence 20, Appl Sequence 61, Appl Sequence 61, Appl Sequence 11, Appl Sequence 11, Appl Sequence 12, Appl Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App Sequence 194, App

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Sequence 137, App Sequence 54, Appl Sequence 54, Appli Sequence 1, Appli Sequence 3, Appli Sequence 30, Appli Sequence 31, Appli Sequence 22, Appli Sequence 22, Appli Sequence 24, Appli Sequence 24, Appli Sequence 27, Appli

Sequence 7, App Sequence 137, 1 Sequence 54, App

Sequence 1, Appli Sequence 32, Appl Sequence 32, Appl Sequence 2, Appli GENERAL INFORMA

Sequence 1, Appli Sequence 2, Appli Sequence 19, Appl

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM nucleic

Run on:

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DB 10; Length 3300,
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US-10-263-153-35

US-10-263-153-51

US-10-263-153-61

US-10-263-153-61

US-10-263-153-13

US-10-263-153-13

US-10-263-153-13

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US-10-801-486-194

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US-10-495-491-1

US-10-495-491-1

US-10-995-491-1

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Publication No. US20030037355A1
GENERAL INPORMATION:
APPLICANT: The Scripps Research Institute
ITTLE OF INVENTION: Methods and compositions to
ITTLE OF INVENTION: Methods and compositions to
ITTLE OF INVENTION: Methods and compositions to
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ITTLE OF INVENTION: MOTHORS. US/09/765,555
CURRENT APPLICATION NUMBER: US/09/765,555
FRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FRAESEQ FOR WINGOWS VERSION 4.0
IEBNGTH: 3300
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US-10-270-176-19
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100.0%; Score 3300;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3300; Conservative 0; Mismatches
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   Sequence 15, Appl
Sequence 18, Appl
Sequence 17, Appl
Sequence 16, Appl
Sequence 1, Applii
Sequence 5, Applii
                                                                                                              2, 2005, 10:29:49; Search time 1309.2 Seconds (without alignments) 16314.373 Million cell updates/sec
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                  GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-09-765-555-16
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TITLE OF INVENTION: Methods and compositions to
TITLE OF INVENTION: Methods and compositions to
TITLE OF INVENTION: Methods and compositions to
TITLE OF INVENTION: Expression in plants
FILE REFERENCE: 27801-20014.40
CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT FILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 15
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                                      US-09-765-555-15

Sequence 15. Application US/09765555
Publication No. US20030037355A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 3300; Conserv
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US-09-765-555-15
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US-09-765-555-18
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; Publication No. US20030037355A1
; GENERAL INFORMATION:
; APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Methods and compositions to
; TITLE OF INVENTION: expression in plants
; FILE REFERENCE: 27801-20014.40
; CURRENT APPLICATION NUMBER: US/09/765,555
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,468
; PRIOR APPLICATION NUMBER: US 60/177,468
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
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ORGANISM: Artificial Sequence
FEATURE:
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1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG 1260 1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320		TGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCAGGCCGGTATAATGGCTGGAATAATGGCTGGTGGAATAATGGCTGGTGGAATAATGGCTGGTGGAATAATGGCGGAATAATGGCGGAATAATGGCGAATAATGGCTGGTTGAAATATGGGCTGGTGAAATAATGGCTGGTTGAAATAATGGCTGGTTGAAATAATGGTGGGAAATAATGATGGGCTGGTTAAATGGGCTGGAAATAATGGGCTGGTAAATGATGAATAATGGGCTGGAAATAATGGGCTGGAAATAATGGGGGAAATAATGAGCTGGTTAAATGGGCTGGAAATAATGAGGGGGAAATAATGAATG	TTCACGA 150	AATCTGG 1	SAAAGAT 1		174			1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAACCTGGGAA 1920 		1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCTGGGGGGTTATGCGTTCAAG 2040 1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040	2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100 	2101 GGTCTGACCTTGCTGGTTGACCTGATTAAAACAAAGAAGACACGACGGACACGGTTAC 2160 2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAACAAACACATGAATGCAGGACACCGATTAC 2160	2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAAACAGCGATGACCATCAACGGCCCGTGG 2220 	2221 GCATGGTCCAACATCGACAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280

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                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Partial sequence of pMal-m4
OTHER INFORMATION: protein ZFPm4
                                                                                                                                                                                                                      97.4%; Score 3215.2; 98.4%; Pred. No. 0;
                                                                                                                                                                                                                                  Pred. No. 0;
0; Mismatches
FILE OF INVENTION: expression in plants
CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 09/620,897
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 3300
                                                                                                                                                                                                                                   Best Local Similarity 98.4
Matches 3247; Conservative
                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                    ; OTHER INFORM US-09-765-555-17
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OTHER INFORMATION: /product = fusion protein MBP Cystatin C BMP-2
FEATURE:
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                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Expression vector pMalc2cchbmp2
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Best Local Similarity 99.2'
Matches 2719; Conservative
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NAME/KEY: CDS
                    SOFTWARE:
SEQ ID NO 1
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GENERAL INFORMATION:
APPLICANT: Wadbach, Gunter
TITLE OF INVENTION: Agent for postoperative use after removal of bone tumors
FILE REPERENCE: 2945-101
CURRENT APPLICATION NUMBER: US/10/257,384A
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: PCT/DE 01/01510
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 19
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	Qy 1201	GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGGG
A 180	Db 1201	GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG
	Oy 1261 Db 1261	1 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGGAGGTCGTAAATCACTGCATAATTCG 1320 
30	Qy 1321	
300	Db 1321	1 IGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTTGCGCCGACATCATAACGGTT 1380
		1 CIGGCAAATATTCIGAAAIGAGCIGITGACAATIAATCAICGGCICGIAIAAIGIGIGGA 1440
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A 480	Qy 1501 Db 1501	1 GCACTTCACCAACAAGGACCATAGATTATGAAACTGAAGAAGGGTAAACTGGTAATCTGG 1560 
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| GENERAL INFORMATION: GENERAL INFORMATION: TITLE OF INVENTION: Method for detecting mut; TITLE OF INVENTION: Method for detecting mut; FILE REFERENCE: 612,406-033 | CURRENT APPLICATION NUMBER: US/10/343,859 | CURRENT APPLICATION NUMBER: PCT/EP01/08127 | PRIOR FILING DATE: 2001-07-13 | PRIOR FILING DATE: 2000-04 |
| NUMBER OF SEQ ID NOS: 52 | SOFTWARE: Patentin Ver: 2.1 | SEQ ID NO 8 | LENGTH: 6648 | LENGTH: 6648 | LENGTH: 6648 | LENGTH: CALLOR OF CA
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                                                                          TITLE OF INVENTION: Method for detecting mutarities of INVENTION: Method for detecting mutarities of INVENTION: Method for detecting mutarities of INVENTION: mutaleotide sequences of INTER REFERENCE: 612,406-033

CURRENT APPLICATION NUMBER: US/10/343,859

CURRENT FILING DATE: 2003-11-24

PRIOR PILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: 10038237.1

PRIOR APPLICATION NUMBER: 10038237.1

PRIOR STUING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin Ver. 2.1
           Sequence 9, Application US/10343859; Publication No. US20040110161A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.8 Matches 2701; Conservative
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Maine, Gregory T.
APPLICANT: Patel, Chandu B.
APPLICANT: Patel, Chandu B.
TITLE OF INVENTION: GINBURG, Sanford R.
TITLE OF INVENTION: GENERATICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REFERENT APPLICATION NUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 7112
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; OTHER INFORMATION: pMBP-G2X-TOXOP30dell1 (52-214aa)
US-10-263-153-40
                                                                                                                                                                                                                                                                                      81.5%; Score 2690.4; 99.8%; Pred. No. 0;
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                                                                                                                                                                                         TYPE: DNA
ORGANISM: Toxoplasma gondii
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Matches 2694; Conservative
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NAME/KEY: CDS
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1711 GCTCMATCTGGCTGTANATCACCCCGACANAGCTTCCTACCACCACTGTT 1860	RESULT 11 US-10-263-153-30 is Sequence 30, Application US/10263153 ; Publication No. US20040067239A1 ; GENERAL INFORMATION: APPLICANT: Abbott Laboratories ; APPLICANT: Patel, Chandu B. ; APPLICANT: Ginsburg, Sanford R. ; APPLICANT: Breil, Chandu B. ; APPLICANT: Ginsburg, Sanford R.
CCGGATCTGCCGTGCTGCGCTGTGCCGATTCAAATACCCGCTGCGATTCAAATGCCCGATAG   CCGGATCTGCCGTGTGCTGCGCTGTGCGATTCAAATGCCGATTCAAATGCCGATAG   To ccgaaAGGCGAAAGGCTGCGCGATTCAAATGCCGCTGCGCGAAATGCTGCTGCGGCGAAATGCTGCTGCGGGGGAAATGCTGCGAAATGCTGCGAAATGCTGCGAAATGCTGCGAAATGCTGCGCGTGCGGGGGAAATGCTGCCGAATGCTGCGAAATGCTGCGAAATGCTGCGAAATGCTGCGAAATGCTGCGAAATACTGCAAATGCTGAAATGCTGCGAAATGCTGAAATGCTGCCAAATGCTGAAATGCTGCAAATGCTGAAATGCTGCAAATGCTGAAATGCTGCAAATGCTGAAATAAAATGCTGAAAATTAAAAATGCTGAAAATTAAAAAATTGCAAATGCTGAAAATTAAAAAATTGCAAATTAAAAAAATTGCAAAAATTCAAAAAAAA	1621 ACCGGAATTAAAGTCACCGTTGAGCATCAAAACTGGAAGGAA

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TITLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REPERENCE: 6984.US.01
CURRENT APPLICATION NUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SEQ ID NO 30
LENGTH: 7259
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                                                                                                                               DB 18;
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches
                                                                                                          TYPE: DNA ORGANISM: Toxoplasma gondii
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; OTHER INFORMATION: pMBP-c2X-ToxoP30del10 (52-284aa)
US-10-263-153-35
                                                                                                                                                                                                                        Score 2690.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.8%;
Matches 2694; Conservative
  SEQ ID NO 35
LENGTH: 7322
TYPE: DNA
ORGANISM: TOXODlasma gondii
FEATURE:
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                                                                     GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC
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Sequence 35, Application US/10263153
Publication No. US2004006723941
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Maine, Gregory T.
APPLICANT: Gineburg, Sanford R.
APPLICANT: Bliese, Timothy R.
TITLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF;
FILE REFERENCE: 6984.US.OI.
CURRENT APPLICATION NUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
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901 ACGATACCGAAGACAGCTCATGTTATATCCGCCGTTAACCACCATCAAACAGGATTTTC 960	GGTGA  - - - GGTGA	CAATA	1081 CGCAAACCGCCTCTCCCGGCGGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT 1140 1081 CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT 1140	1141 CCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA	1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGGG 1260 	1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGTCGTAAATCACTGCATAATTCG 1320 	1321 IGTGGCTGAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 1380 1321 IGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 1380	1381 CTGGCAARTATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440 	1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 	1501 GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGGAAACGTAAACTGGTAATCTGG 1560 	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT 1620 	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT 1680 	1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACGACGGCTTTGGTGGCGCTAC 1740	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAGCGTTCCAGGACAGCTGTAT 1800 	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGACCCGCCAAAAACCTGGGAA 1920 	1921 GAGATCCCGGCGCTGGATAAGAACTGAAGCGAAAGGTAAGACGCGCTGGTGTTCAAC 1980 

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120 120 GIGICTCTTATCAGACCGTTCCCCGCGTGGTGAACCAGGCCAGGCCACGTTTCTGCGAAAA 180 180 240 240 300 360 1020 1140 300 360 420 420 480 9 480 540 540 900 99 9 900 9 720 720 780 780 840 840 900 900 960 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG GIGICICTIAICAGACCGITICCCGCGTGGTGAACCAGGCCAGCCACGTITCTGCGAAAA ACGCGCCGTCGCAAATIGTCGCGGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG CGCGGGAAAAAGTGGAAGCGGCGATGGGGGAGCTGAATTACATTCCCAACCGCGTGGCAC AACAACTGGCGGCCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGC TGGTGGTGTGGTAGAACGAAGCGCGTCGAAGCCTGTAAAGCGGCGGCGGTGCACAATC TTCTCGCCCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA TIGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA 481 Triccheredanderieceredanderrecesecerrarrecreanstrecesea CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCCATTAAGTTCTGTCTCGG CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG TGCGCGCCATTACCGAGTCCGGGCTGCGCGTGCGGATATCTCTCGGTAGTGGGATACG CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAAGCTGC ATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACACAGGTTT ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 

	CCGAACAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA	CCGAACAAGGGCTGGCAAAAGGGTTCCTCGAAAACTGTCTGCTGACTGA	GAAGCGGTTAATAAAGACAAACCGCTGGGGGCGCGTGAAGCGCTGAAGTCTTACGAGGAAGAG 2460	GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG 2460	TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520	TIGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAACGCCCAGAAAGGTGAAATCATG 2520	CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGGTGATCAACGCC 2580	CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGGTGCGTACTGCGGTGATCAACGCC 2580	GCCAGCGGTCGTCAGACTCTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640	GCCAGCGCTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGAGTAATTCGAGCTCG 2640	AACAACAACAACAACAATAACAACAACCTCGGGATCGAGGGAAGGATTCAGAATTC 2700	AACAACAACAATAACAATAACAACAACATCGGGATCGGGGAAGGGATTTCAGAATTC 2700	
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                                                                                                                                                             July 31, 2005, 14:24:04 ; Search time 1094.6 Seconds (without alignments) 17846.836 Million cell updates/sec
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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1992. .3042
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076, 3141
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WO200152620-A2.

26-JUL-2001.

19-JAN-2001; 2001WO-US001817

21-JAN-2000; 2000US-0177468P. 21-JUL-2000; 2000US-00620897. (SCRI ) SCRIPPS RES INST. (SYGN ) SYNGENTA AGRIC DISCOVERY INC Barbas CF, Stege JT, Guan X, Dalmia B;

WPI; 2001-465325/50. P-PSDB; AAE06000. New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the target gene.

Example 4; Page 138-139; 156pp; English.

The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) which is capable of specifically binding to a target mucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target mucleotide sequence, where the expression of the target gene in the plant cells is modulated. The ZFP binding to the target plant cells is modulated. The ZFP and fusions of the ZFP proteins are useful plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with paticular expression of the target gene. The present DNA sequence is the partial sequence of pMal-ml and ZFPPmIDNA

ö GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1020 120 180 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120 180 240 300 300 360 420 420 480 480 540 540 600 900 099 99 720 720 780 780 840 900 840 900 CGACACCATGGAATGGTGCAAAACCTTTGGGGTATGGCATGATAGGCGCCGGAAGAGA 60 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG GTGTCTCTTATCAGACCGTTTCCCGCGTGGAACCAGGCCAGGCCACGTTCTGCGAAAA CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA GTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGGCCACGTTTCTGCGAAAA 301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA TIGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC TGGTGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATC TTCTCGCGCAACGCGTCAGTGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCCA TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG CGGAACGGGAAGGCGACTGGGAGTGCCATGTCCGGTTTTCAACAAACCAAGCAAATGCTGA ATGAGGCATCGTTCCCACTGCGATGCTGGCTACCAACGATCAGATGGCGCTGGGCGCAA 781 ATGAGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA Gaps ; 0 DB 4; Length 3300; Sequence 3300 BP; 847 A; 874 C; 876 G; 703 T; 0 U; 0 Other; 0; Indels 100.0%; Score 3300; 100.0%; Pred. No. 0; 0; Mismatches Best Local Similarity 100. Matches 3300; Conservative Н 121 61 61 181 181 241 241 301 361 361 421 481 541 541 601 721 Query Match 121 421 481 601 661 661 721 781 841 901 106 841 961 XS Dp g ð ò ద ò Db ઠે g ò 엄 ò ద 8 g 8 8 8 Dp qq ò 8 g ઠે Ωp 8 6 6 6 ઠે a à

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21-JUL-2000; 2000US-00620897.
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                                                                P-PSDB; AAE06002
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modulation; plant technology; agriculture; ds.
CCAGAATGTGGCAAGTCTTTCTCTCGGTCTGACAATCTCGTCCGGCACCAACGTACTCAC
          3181 CCAGAATGTGGCAAGTCTTTCTCTCGGTCTGACAATCTCGTCCGGCACCAACGTACTCAC
                                    3241 ACCGGTAAAAAACTAGTGGCCAGGCCGGCAGTACCGGTACGACGTCCGGACTACGCT
                            ACCGGTAAAAAAACTAGTGGCCAGGCCGGCCAGTACCGTACGACGTTCCGGACTACGCT
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bound moiety= "F3-b1 primer"
953. 3021
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bound_moiety= "F2-f primer"
916. _2973
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                                                                                                                   Partial sequence of pMal-m2 and ZFPm2 DNA.
                                                                                                                                                                                      protein"
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                                                                                                                                                                  location/Qualifiers
                                                                                                                                                                                      "ZFPm2
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3119. .3192
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168. .3225
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZPP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZPP binding to the target modulates equence, where the expression of the target gene in the plant cells is modulated. The ZPP and fusions of the ZPP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZPP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-m2 and ZPPm2 DNA
                                                                                                                                                                                                                                                                                                                     New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
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100.0%; Pred. No. 0;
live 0; Mismatches
                                                                                                                           Dalmia B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; Page 140-142; 156pp; English
(SCRI ) SCRIPPS RES INST.
(SYGN ) SYNGENTA AGRIC DISCOVERY INC.
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Best Local Similarity 100.
Matches 3300; Conservative
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1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carget gene.
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             2760
                                         CGGGAATGTGGTAAGTCCTTCTCTCAGAGCTCTCACCTGGTGCGCCACCAGCGGTACCCAC 2820
                                                                                                                                                                                                                                                                                                    CCAGAATGTGGCAAGTCTTCTCTCGGTCTGACAATCTCGGCCGCCACCAACGTACTCAC 3240
                                                                                                                                                                                                                                                                                                                3241 ACCGGTAAAAAACTAGTGGCCAGGCCGGCCAGTACCGTACGACGTTCCGGACTACGCT 3300
                                                                                                                                                                                                                                                                                                                                                     3241 ACCGGTAAAAAAACTAGTGGCCAGGCCGGCCAGTACCCGTACGACGTTCCGGACTACGCT 3300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc finger protein; ZFP; gene expression; metabolic pathway regulator; modulation; plant technology; agriculture; Ap3; APETALA3; ds.
2821 ACGGGTGAAAAACGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGCCAGTCCAGCAAC
                                                                                      ACGGGTGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGCCAGTCCAGCAAC
                                                                                                                      CTGGTGCGCCATCAACGCACTCATACTGGCGAGAAGCCATACAAATGTCCAGAATGTGGC
                                                                                                                                               AAGTCTTTCTCTCGGTCTGACAATCTCGTCCGGCACCAACGTACTCACACCGGGGAGAAG
                                                                                                                                                                                   CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCAGCCGCAGCGATAACCTGGTGCGCCAC
                                                                                                                                                                                                       CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCAGCCGCAGCGATAACCTGGTGCGCCAC
                                                                                                                                                                                                                         CAGCGTACCCACACGGGTGAAAAACCGTATAAATGCCCAAGAGTGCGGCAAATCTTTTAGC
                                                                                                                                                                                                                                             3061 CAGCGTACCCACACGGGGGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGC
                              CCGGAATGTGGTAAGTCCTTCTCAGAGCTCTCACTGGTGCGCCCACCAGCGTACCCAC
                                                                                                         CTGGTGCGCCATCAACGCACTCATACTGGCGAGAAGCCATACAAATGTCCAGAATGTGGC
                                                                                                                                                                 AAGTCTTTCTCTCGGTCTGACAATCTCGTCCGGCACCAACGTACTCACACCGGGGAGAAG
                                                                                                                                                                                                                                                               CAGGCCGGCCACCTGGCCAGCCATCAACGCACTCATACTGGCGAGAAGCCATACAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'trans1_except= (pos:3124. .3126, aa:Ser)
'trans1_except= (pos:3127. .3129, aa:Ser)
'trans1_except= (pos:3136. .3138, aa:Val)
'note= "CDS does not include start and stop codon"
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*tag= b
bound_moiety= "F1-f2 primer"
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bound_moiety= "F1-f1 primer"
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/*tag= d
/bound_molety= "F2-b primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial sequence of pMal-Ap3 and ZFPAp3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product= "ZFPAp3 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           AAD11592 standard; DNA; 3300 BP.
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) Which is capable of specifically binding to a target uncleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target uncleotide sequence, where the expression of the target gene in the plant cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-Ap3 (APETALA3) and ZFPAD3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 97.8%; Score 3226.4; DB 4; Length 3300; Best Local Similarity 98.6%; Pred. No. 0; Matches 3254; Conservative 0; Mismatches 46; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3300 BP; 853 A; 872 C; 876 G; 699 T; 0 U; 0 Other;
                                                                                                                                                                                          *tag= g
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                                                                                                                                                                                                                                                                                        *tag= h
bound moiety= "F4-f2 primer"
1022. _3102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bound_moiety= "F6-b1 primer"
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/bound_moiety= "F6-b2 primer"
                                                                                                                            bound moiety= "F3-b1 primer"
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'*tag= e
'bound_moiety= "F2-f primer"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SYGN ) SYNGENTA AGRIC DISCOVERY INC.
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/bound_moiety= "7
3076. .3141
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3168. .3225
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21-JUL-2000; 2000US-00620897.
                                                          .2973
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Gaps

Page 7

CCCGAACCGCCACCCCCCCCCCCCCCTTACACTAAATGCAGCTGCACACACA	1861 GAAGCGTTATCCTGGGGTACCTTACAACGGCAAGCTGATTGCTTACCCGGATCGCTGTT 1860 1861 GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCCGCCAAAACCTGGGAA 1920 1861 GAAGCGTTATCGCTGATTATAACAAGATCTGCTGCCGAACCCGCCAAAACCTGGGAA 1920 1921 GAGGTCTTATCGCTGGTAAAGAACTCGAAGGCGAAACCCGCCAAAAACCTGGGAA 1920 1921 GAGATCCCGGCGCTGGATAAAGAACTCGAAGGCGAAAGGCGCCCCAAAAACCTGGGAA 1920 1981 CTGCAAGAACCGTAAAAGAACTCGAAGGCGAAAGGCGCGCTGATTGCTTCAAC 1980 1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGAGGCGCGCTTATGCGTTCAAC 2040 2041 TATGAAAACGGCAAGTACGACTGATGCTGCTGCTGCTGCGGGGTTATGCGTTCAAG 2040 2041 TATGAAAACGGCAAGTACGACTTAAAGACGTGGTGGCGCGGAAAGCC 2100 2041 TATGAAAACGGCAAGTACGACTTAAAAACCGTGGGCGCGGAAAGCC 2100 2041 TATGAAAACGGCAAGTACGACTTAAAAACCGTGGGCGCGGAAAGCC 2100 2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAACAAGAATAACGCTGGCGCGAAAGCC 2100 2101 GGTCTGACCTTCCTGGTTGACTAAAAACAAACAAGAAGAAGACCGTTAACCGTTACCTGGTTACCTGGTTACCTGGTTACCTGGTTACTAAAAACAAAC
8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6	8 6 8 6 8 6 8 6 8 6 8
	121   CGGAACGGGAACCCCACTGCGATTTTCAACAACCATGCAATGCTGA 780   TATCAGGGAACGCACTGCGAATGCTGA 780   TATCAGGGCATCCTTCCCACTGCGATGCTACCAATGCTGCAATGCTGA 840   TATCAGGGCATCGTTCCCACTGCGATGCTGCTACCACGATGCGAGCGCTGGGCCAA 840   TGCGCGCCATTACCGAGTCGCTGGTTGGTGGGATACTGGTGGGGATACG 900   TGCGCGCCATTACCGAGTCCGGGTTGGTGGGGATACTGGTGGGATACG 900   TGCGCGCCATTACCGAGTCCGGGTTGGTGGGGATATCTCGGTAGTGGGATACG 900   TGCGCGCCATTACCGAGGTCCGGGTTGGTGGGGATATCTCGGTAGTGGGATACG 900   TGCGCGCCATTACCGAGGCTCGTTGGTGGGGATACCGGGGATACC 900   TGCGCGCCATTACCGAGGCTCGTTGGTGGGATACCGGGGATACCGGGGATACCGGGGATACCGGGGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG

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metabolic pathway regulator; ds.
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/*tag= f
/bound_moiety= "F3-b1 primer"
/*tag= 3933, 3021
/*tag= g
/bound moiety= "F3-b2 primer"
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1770. .2850
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2824. _2889
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bound_moiety= "F4-f1 primer"
076. 3141
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bound moiety= "F4-f2 primer"
022. 3102
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/bound_moiety= "F2-b primer"
2867. .2940
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bound_moiety= "F5-b primer"
119. 3192
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bound moiety= "F5-f primer"
168. 3225
                                                                                                                              Zinc finger protein; ZFP; gene expression; modulation; plant technology; agriculture;
                                                                                                       Partial sequence of pMal-m4 and ZFPm4 DNA
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC.
                                                                                                                                                                                              Location/Qualifiers
2719. .3270
                               BP.
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/bound_moiety= "
3205. .3273
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                               AAD11591 standard; DNA; 3300
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21-JUL-2000; 2000US-00620897.
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                                                                                (first entry)
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                                                                                                                                                                    Jnidentified
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                                                       AAD11591;
     RESULT 4
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                                                                                                  TIGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520
                                                                                                                                                                                                                   2461 TIGGCGAAAGATCCACGTATTGCCGCCACATGGAAAAGGCCCAGAAAGGTGAAATCATG 2520
                                                                                                                                                                                                                                                    CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGC 2580
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                                                                                                                                                    GAAGCGGTTAATAAAGACAAAACGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
                      2221 GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
                                                   AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT
                                                                            AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT
                                                                                                                                                                                                                                                                   2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
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New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of Example 4; Page 145-147; 156pp; English 2001-465325/50 P-PSDB; AAE06004 target gene

the

The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ETP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZPP binding to the target mucleotide sequence, where the expression of the target gene in the plant cells is modulated. The ZPP and fusions of the ZPP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZPP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-m4 and ZPPm4 DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes human Cdc25C phosphatase, and was expressed in Escherichia coli. It is used to make fusion proteins with Escherichia coli maltose binding protein (MBP). The specification describes fusion proteins of MBP and one of Cdc 25B1, 25B2, 25B3 and 25C. Cdc phosphatases are involved in activation of cyclin-dependent kinases (CDK) that control cell division. The fusion proteins are used to identify modulators of the specified human Cdc phosphatases, potentially useful for regulation of cell division. They are also for studying physiological or physiopathological activities of Cdc phosphatase
                                                                                                                                                                                                                                                                                                                                                                            fusion protein of maltose-binding protein and Cdc phosphatase, useful identifying phosphatase modulators for regulating the cell cycle.
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             ltose binding protein; MBP; Cdc25C phosphatase;
Cdc25B3; cyclin-dependent kinase; CDK; cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCACGCTTTCTGCGAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
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82.0%; Score 2705.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2707; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                Prevost
                                                                                                                                                                                                                                                                            (SCRC ) SCRAS SOC CONSEILS RECH & APPL
                                                                                                                                                                                                                                                                                                              Ducommun B,
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 9-13; 56pp; French.
                                                                                                                                                                                                          14-DEC-1999; 99FR-00015722.
30-MAY-2000; 2000FR-00006883.
21-SEP-2000; 2000FR-00012008.
                                                                                                                                                                             13-DEC-2000; 2000WO-FR003496
                 maltose
                                                                                                                                                                                                                                                                                                             Goubin-Gramatica F,
                                                                                                                                                                                                                                                                                                                                             WPI; 2001-398152/42
                 protein; mail Cdc25B2;
                                                                                                                WO200144467-A2
                                                                                Homo sapiens.
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               Fusion pro
Cdc25B1; (
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2641 AACAACAACAATAACAATAACAACACCTCGGGATCGAGGGAAGGATTTCAGAATTC 2700
                                                                                                                                                                                                                                                                                                                                                                                                        Cdc25C phosphatase, amine; Cdc25 phosphatase; spontaneous alopecia; alopecia; proliferative disease; parasitic disease; viral infection; neurodegenerative disease; myopathy; anglogenesis; psoriasis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents pMAL-HsCdc25C, a plasmid encoding human Cdc25C phosphatase. The specification describes the use of aryl-
substituted secondary or tertiary amines for the production of medicaments for inhibiting Cdc25 phosphatases, especially Cdc25C phosphatases. The amines of the invention are used for treating sobntaneous alopecia or alopecia induced by exogenous products or radiation. They are also used for treating tumoural or non-tumoural proliferative diseases, parasitic diseases, viral infections, proliferative diseases are e.g. anglogenesis, psoriais or restenosis. Proliferative diseases are e.g. anglogenesis, psoriais or restenosis. The amines are also useful for inhibiting the proliferation of microorganisms (especially yeasts) and in the treatment of all disorders conventionally treated with vitamin K or its derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cdc25 Phosphatase inhibiting medicaments, useful e.g. for treating tumor diseases, viral infections, neurodegenerative disease or alopecia, containing new or known aryl-substituted amines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8101 BP; 2127 A; 1987 C; 2121 G; 1866 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
/note= "encodes maltose binding protein (MBP)"
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/*tag= a
/note= "ORF of human Cdc25C"
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                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of pMAL-Hs Cdc25C.
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                                                                                                                                           GGATCCTCT
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Homo sapiens
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GCACTTCACCAACAAGGACCATAGATTATGAAAATCGAAGAAGGTAAACTGGTAATCTGG 1560
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                                       ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT
                                                                      1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT
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Query Match         82.0%;         Score 2705.8;         DB 6;         Length 8101;           Best Local Similarity         99.9%;         Pred. No. 0;         Action of the conservative         0;         Mismatches         2;         Indels         0;         Gaps         0;           Action of Conservative         0;         Mismatches         2;         Indels         0;         Gaps         0;           Action of Conservation of Conser	GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG [	TTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGCCACGTTTCTGC AAAAATGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGT 	241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC 300		361 TGGTGGTGTCGATGGTAGAACGAGGCGTCGAAGCCTGTAAAGCGGGCGTGCACAATC 420 421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 480 421 TTCTCGCGAACGCGTCAGTGGCTGATTAACTATTACTATTAATATAATAATAATAATAATAATA	TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA	CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC	601 IGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 660 	661 CGCGTCTGCGTCTGGCTGGCTTGAATATCTCACTCGCAAACAAA	721 CGGAACGGGAAGGCGACTGGAGTGCCATGTTCCGGTTTTCAACAAACCATGCAAATGCTGA 780 	781 ATGAGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA 840 	841 TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG 900 	901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 960 	961 GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1020 

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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding MBP-ToxoP30del8(82-294aa) fusion protein
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(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
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The invention relates to a purified P30 antigen (1) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30del3C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-TOxO30del3C(52-300aa), MBP-TOXO30del4C(52-294aa) and MBP-TOXO30MIX1 fusion proteins. (1) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (1) and detecting the presence of (1)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-TOXOP30 fusion protein of the invention.
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                                                                                                                                                                                                                                                                                   Novel purified polypeptide having sequence identity to amino acid sequence of F93 antigen of Toxoplasma gondii e.g. Toxo30de13C, Toxo30de12C, Toxo30de12C, Toxo930 MIXI, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
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Matches 2694; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIXI sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acid sequence in amino acid sequence of Toxo30del3C P30 antigen sequence in substituted with alanine, or comprising the amino acid sequence converting the amino acid sequence chosen from MBP-Toxo30del3C(52-300aa), MBP-Toxo30del4C(55-294aa) and MBP-Toxo30miXI fusion proteins. (I) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo330del2C, Toxo930 MIX1, useful for detecting presence of IgM or IgG
                                                                                     P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP10 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; da; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATGATGGCCCCGGAAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.5%; Score 2690.4; DB 12; Length 7322; 99.8%; Pred. No. 0; ative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7322 BP; 1887 A; 1844 C; 1934 G; 1657 T; 0 U; 0 Other;
                                          DNA encoding MBP-ToxoP30del10(52-284aa) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bliese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ginsburg SR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies to Toxoplasma gondii
                                                                                                                                                                                                                                                                                                                                           02-OCT-2002; 2002US-00263153
                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2002; 2002US-00263153
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                            (MAIN/) MAINE G T.
(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GT, Patel CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2004-304563/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 2694; Conserv
                                                                                                                                                                              Toxoplasma gondii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG
                                                                                                                                                                                                                                                                                                2641 AACAACAACAACAATAACAATAACAACATCGGGGATCGGGGAAGGATTTCAGAATTC
GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
                                                                              TTGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAAAGCCCCAGAAAGGTGAAATCATG
                                                                                                                                                       2581 GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG
                                                         TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG
                                                                                                                              CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
                                                                                                                                                                                                       GCCAGCGCTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding MBP-ToxoP30del4C(52-294aa) fusion protein.
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(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
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                                                                                                                                                                                                                                                                                                                     ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT
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                                                                                            CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA
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                                    TGTCGCTCAAGGCGCACTCCCGTTCTGGATATGTTTTTTTGCGCCGACATCATAACGGTT
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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30de12C and ToxoP30 MIXI sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30de13C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-Toxo30de13C(52-294as) and MBP-ToxO30MIXI fusion proteins. (I) is useful for detecting the presence of IGM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IGM antibodies with a composition comprising (I) and detecting the presence of (I)/IGM antibody complexes. The present sequence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.
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                                                                                                                                                           Novel purified polypeptide having sequence identity to amino acid sequence of F930 antigen of Toxoplasma gondii e.g. Toxo30de112C, Toxo2030 MIXI, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
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99.8%; Pred. No. 0;
ive 0; Mismatches
                                            Ginsburg SR,
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Matches 2694; Conservative
                                            Patel CB,
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P-PSDB; ADO23599.
(BLIE/) BLIESE T R.
                                            Maine GT,
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                           TATGAAAACGGCAAGTACGACATTAAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
                                                                                                                    GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
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TATGAAAACGCCAAGTACGACATTAAAGACGTGGCCGTGGATAACGCTGGCGCGAAAGCG
                                                                                                                                                                                         TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
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                                                                                           GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACACATGAATGCAGACACCGGATTAC
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA encoding MBP-ToxoP30del3C(52-300aa) fusion protein.
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(GINS/) GINSBURG S R.
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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Matches 2694; Conservative
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GINSBURG S R.
BLIESE T R.
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P-PSDB; ADO23640.
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Synthetic.
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                         GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
                                                                                                                                                 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
                                                                                                             TTGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAAGGCCCAGAAAGGTGAAATCATG
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.
                                                                                                            CGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCGGAAGAGA
                                                                                                                                  GTCAATTCAGGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG
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1140 1380 1440 1440 1500 1500 1620 1680 1020 1020 1080 1140 1200 1200 1260 1260 1320 1320 1380 1560 1560 1620 1680 1800 1800 1860 1920 1920 1980 2040 1860 960 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA GCACTTCACCAACAAGGACCATAGAATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG CTGCAAGAACCGTACTTCACCTGGCTGATTGCTGCTGCTGAGGGGGTTATGCGTTCAAG ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCAATA CGCAAACCGCCTCTCCCCGCGCGTTGCATTCATTAATGCAGCTGGCACGACAGGTTT GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGTGCACCAATGCTTCTGGCG TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAAATTCG TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAAACGGTT CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGAGGGA GCACTTCACCAACAAGGACCATAGGATATGAAAATCGAAGAAGGTAAACTGGTAATCTGG ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAATTCGAGAAAGAT GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACGCGACCGCTTTGGTGGCTAC GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACTGTGGGAA GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAACCACCCTGGCGCCCAATA CGCAAACCGCCTCTCCCCGCGCTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG TCAGGCAGCCATCGGAAGCTGTGGCTGTGCCAGGTCGTAAATCACTGCATAATTCG TGTCGCTCAAGGCGCACTCCCGGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACCACGACCGCTTTGGTGGCTAC GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC

Bliese TR;

Ginsburg SR,

PATEL C B. GINSBURG S R BLIESE T R.

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Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, Toxo930 MIX1, useful for detecting presence of IgM or IgG
                                                                                                                                               Example 5; Fig 33; 114pp; English
                                                                                                                           antibodies to Toxoplasma gondii.
                                                Maine GT, Patel CB,
                                                                 WPI; 2004-304563/28
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                                  2041 TATGAAAACGCCAAGTACGACATTAAAGACGTGGGCGTGGGTTAAACGCG
                                                            GOTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC
                                                                             2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
                                                                                                                                          GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding MBP-ToxoP30MIX3 fusion protein.
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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30del3C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence of Toxo30del3C P30 antigen sequence of sequence of Toxo30del3C (52-294aa) and MBP-Toxo30del3C (52-30daa), MBP-Toxo30del4C(52-294aa) and MBP-Toxo30MIX1 (Is useful for detecting the presence of IgM contacting the test sample suspected of containing the IgM antibodies contacting the test sample suspected of containing the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-CC ToxoP30 fusion protein of the invention.
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Pred. No. 0;
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99.8%;
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Matches 2694; Conservative
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The invention relates to a purified P30 antigen (I) chosen from 3 fully efficient Toxo30del3C, Toxo30del2C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30del3C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-TOxO30del3C(52-100aa), MBP-TOXO30del4C(52-294aa) and MBP-TOXO30MIX1 antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-TOXOP30 fusion protein of the invention.
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                                                                                                                                       P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30de13C, Toxo30de12C, ToxoP30 MIX1, useful for detecting presence of IgM or antibodies to Toxoplasma gondii.
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                                                                                                          DNA encoding MBP-ToxoP30del2(52-311aa) fusion protein
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                    DNA; 7403
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                                                                             01-JUL-2004 (first entry)
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PATEL C B.
GINSBURG S R.
BLIESE T R.
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P-PSDB; AD023595.
                    standard;
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STRANDEDNESS: double
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Sequence 785, App
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Sequence 3, Appl
Sequence 62, Appl
Sequence 784, App
Sequence 784, App
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Sequence 2, Appli
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Sequence 5, Appli
Sequence 12, Appli
Sequence 18, Appl
Sequence 35, Appli
Sequence 35, Appli
Sequence 35, Appli
                                                                                                                                  2, 2005, 10:29:49 ; Search time 352.4 Seconds (without alignments) 15322.682 Million cell updates/sec
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!: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-027-169-3

US-09-640-882-2

US-09-640-882-3

US-08-148-675A-2

US-08-148-675A-2

US-08-148-675A-2

US-08-148-675A-2

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US-08-148-675A-18

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                                                                                                OM nucleic
                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                       Run on:
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GS-001-036-1

GS-00-971-036-1

S-G-quence 1, Application US/08971036

FRAPLICANT Actwood, Michael R

APPLICANT Hurst, David N

APPLICANT Hurst, David N

APPLICANT Hurst, David N

APPLICANT Hurst, Bayham Trony M

APPLICANT: Wilson, Francis X

TITIZE OF INVENTION: Amino Acid Derivatives

NORRESPONDENCE ADDRESS:

CORRESPONDENCE HORBESS:

CORRESPONDENCE HORBESS:

STREET: 340 Kingsland Street

CITY: NULL BY

CONPITER N.3.

CONPITE: N.3.

CONPITE: N.4.

CONPUTE: IBW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Ploppy disk

COMPUTE: IBW PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PLOPPY DAVA:

APPLICATION NUMBER: US/08/971,036

FILING DARE: 14-NOV-1997

CURRENT APPLICATION DAVA: 530

PRIOR APPLICATION NUMBER: GB 9623900.2

FILING DARE: 18-NOV-1996

ATTOONEY/ACENT INPORMATION:

NAME: BRENEWIC/DOCKET NUMBER: BS 22

REGISTRATION NUMBER: 18-NOV-1996

ATTOONEY/ACENT INPORMATION:

TELEFRONGE (1973) 235-2363

TELEFRONGE (1973) 235-2363

TELEFRONGE (1973) 235-2363

TELEFRONGE (1973) 235-2363

TYPE: INDUCTION CITCULAR

MOLECULE TIPE: DNA (9enomic)

WOLECULE TIPE: DNA (9enomic)
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1021 AGGGCAATCAGCTGTTGCCCGATTCATTAATGCACCTGGCCCCAATTA 106   1081 CGCAAACCGCCTCCCCCGCGGTGCCCAATTCATTAATGCACCTGGCACCACACGTT 114   1081 CGCAAACCGCTTCCCCCGCGGTGCCCAATTCATTAATGCACCTGCACCACACGTT 114   1141 CCCCCCTCCGCCGCCCCCCCGCGTCCAATTCAATCCACCTGCACCACGTT 114   1141 CCCCCCTCCCCCCCCCCCCCCCCCCCCCCCCCCC	2041 INTRADAMCGGCAAGTACGACATTAAAGACGTGGGGTGGATAACGCTGGCGCGAAAGCG 2100 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGCGTTGGATAACGCTGGCGGAAAGCG 2100 2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACAAGAAGAGAGAG
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Matches 2700 S Matches 2700 S Matches 2700 S Matches 2700 S Matches 2700 Matches 27	QY         961 GCCTGCTGGGGCAACCAGGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1020           Db         961 GCCTGCTGGGGAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1020           QY         1021 AGGGCAATCAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGGCGCCCCAGTA 1080

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   RAN 4430/073
REFERENCE/DOCKET NUMBER: RAN
TELECOMONINICATION INFORMATION:
TELEPHONE: (973) 235-4387
TELEFAX: (973) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7475 base pairs
                                                                                                                                   TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                        TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                            Best Local Similarity
Matches 2700; Conserv
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US-09-096-570-1
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                 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAAACAGCGATGACCATCAACGGCCCGTGG
                                                                                             GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
                                                                                                                                                                                                                                                                               GAAGCGGTTAATAAAAGACAAACCGCTGGGTGCCCTAGCGCTGAAGTCTTACGAGGAAGAG
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                                                                                                                                        AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT
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ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
RPLING CATION NUMBER: US/09/096,570
FILING CATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Attwood, Michael R
APPLICANT: Huret, David N
APPLICANT: Hones, Philip S
APPLICANT: Gones, Philip S
APPLICANT: Ray, Paul B
APPLICANT: Raynham, Tony M
APPLICANT: Wilson, Francis X
TITLE OF INVENTION: Amino Acid Derivatives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Hoffmann-La Roche Inc
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/971,036
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/09096570; Patent No. 6018020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 38522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Nutley
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1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCTAAGAGCGCGCTGATGTTCAAC 1980	2101 2101 2101 2161 2161		Qy         2341 CCGAACAAAGAGTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGATGAAGGTCTG         2400           Db         2341 CCGAACAAAGAGTTCCTCGAAAACTATCTGCTGATGATGAAGGTCTG         2400           Qy         2401 GAAGCGGTTAATAAAGACAAACGGTGCTGGGTGCCTAAGGTTTACGAGGAAGAG         2460           Db         2401 GAAGCGGTTAATAAAAGACAAACCGCTGGGTGCCGTAGCGCTCAAGTCTTACGAGGAAGAG         2460           Db         2401 GAAGCGGTTAATAAAAGACAAACCGCTGGGTGCCGTAACGCTGAAGTCTTACGAGGAAGAG         2460	Oy 2461 TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520	QY         2581         GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG         2640           Db         2581         GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCCAGCTCG         2640           QY         2641         AACAACAACAACAATAACAATAACAACAACAACAACGGGAAGGAA	RESULT 3 US-09-265-617B-1 Sequence 1, Application US/09265617B Sequence 1, Application US/09265617B Patent No. 6372883 GENERAL INFORMATION: APPLICANT: Attwood, Michael R. APPLICANT: Hurst, David N. APPLICANT: Ray, Paul B. APPLICANT: Raynham, Tony M. APPLICANT: Milson, Francis X. TITLE OF INVENTION: Antiviral Medicaments FILE REFERENCE: 20052 antiviral medicaments CURRENT APPLICATION UNMBER: US/09/265,617B CURRENT FILING DATE: 1999-03-10 PRIOR APPLICATION NUMBER: GB9806815.8 PRIOR APPLICATION NUMBER: GB9806815.8 NUMBER OF SEQ ID NOS: 24 SOFTWARE: PatentIn Ver. 2.0
### ################################	GCCTGCTGGGGCAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA AGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAACAACACCCTGGCGCCCAATA	1141 CCCGACTGGAAAGCGGCGGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT 1140 1141 CCCGACTGGAAAGCGGCAGTGAGCGCAATTAATGTGAGTTAGCTCATTAG 1200 1141 CCCGACTGGAAAGCGGCAGTGAGCGCAATTAATGTGAGTTAGCTCATTAG 1200 1201 GCCGACTAGTAGACAGCGCTATCATCACAGCACGTCACCATTAGCTCGCG 1260 1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACGTCACCAATGCTTCTGGCG 1260 1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACGTGCACGATGCTTCTGGCG 1260	1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTAGCTGTAAATCACTGCATAATTCG 1320	TGTGTGGA		1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGGAA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1264 GCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                  1564 GACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGT
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                                                                                                                                                                                                                                                                                                           DB 3;
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                                                                                                                                                                                                              ; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "pEM delta R.adj to 1"
US-09-027-169-3
                                                                                                                                                                                                                                                                                                       Query Match
43.0%; Score 1417.6;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1455; Conservative 0; Mismatches
   NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 5789-3
TELECOMMUNICATION INFORMATION:
TELEPAX: 919 801 3175
TELEPAX: 919 801 3175
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 5926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
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CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CRAIG, NANCY L.
TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
TITLE OF INVENTION: ATP-DEPENDENT TRANSPOSITION PROTEINS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Anne Brown (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave.
CITY: Raieigh
STATE: NC
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COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIPECATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/09027169; Patent No. 6420524; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 27608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  Length 5201;
                           10; Indels
  DB 4;
 Score 1362; DB
Pred. No. 0;
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41.3%; initarity 99.1%; l
Conservative 0,
 Query Match
Best Local Similarity
Matches 1380; Conser
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| Sequence 2, Application US/09640882
| Patent No. 6720142
| GENERAL INFORMATION:
| APPLICANT: Hall, Barry G. |
| TITLE OF INVENTION: RESISTANCE GENES AND USE THEREOF TO SCREEN FOR DRUG |
| TITLE OF INVENTION: REPETCACY |
| FILLE REFERENCE: 176/60851 |
| CURRENT APPLICATION NUMBER: US/09/640,882 |
| FRICR APPLICATION NUMBER: 06/149,813 |
| PRIOR APPLICATION NUMBER: 60/149,813 |
| PRIOR PILLING DATE: 1999-08-19 |
| NUMBER OF SEQ ID NOS: 17 |
| SOFTWARE: PatentIn Ver. 2.1
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GAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCTGGGCGCAATG
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                                      CGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGAC
                                                      CTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAG
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: pACSE2
US-09-640-882-2
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             2683 GIGICTCITALCAGACCGTTTCCCCGCGTGGTGAACCAGGCCAGCCACCTTTCTGCGAAAA
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Sequence 5, Application US/08778717

Patent No. 6602689

GENERAL INFORMATION:

APPLICANT: UENO, EIICHI
APPLICANT: OKADA, MASAHISA

TITLE OF INVENTION: EXPRESSED FROM SAID FUSED PROTEIN

TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
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TOPOLOGY:
TOPOLOGY:
ORIGINAL SOURCE:
ORGANISM: B. COLI
STRAIN: BL21 (DE3)
PUBLICATION INFORMATION:
AUTHORS: NOBUTUKI FUJII ET AL,
AUTHORS: PROBUTUKI FUJII ET AL,
TITLE: FROM SAID FUSED DNA SEQUENCE, AUTHORS AND METHOD OF
TITLE: EXPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 4557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: ELPOPY disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/778,717

FILING DATE: 12-DEC-1996

CLASSIFTCATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JB 35225/1995

FILING DATE: 28-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: OBLOM, NORMAN F:

REGISTRATION NUMBER: 2084-031-0

TELERDANE: 703-413-3000

TELERDANE: 703-413-3000

TELERDANE: 703-413-220

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 4557 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
                                                  1383 GGCAAATATTCT 1394
                                                                                      2244 GGCAAATATTCT 2255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-778-717-5
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US-08-487-283A-18/c
Sequence 18, Application US/08487283A
Perent No. 635545
GENERAL INFORMATION:
APPLICANT: Evans, Mark J.
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                                                                                                                                                      Sequence 2, Application US/08148675A
Patent No. 550121
GENERAL INFORMATION:
APPLICANT: SKETZA, ATNE; SCHMIGL, Thomas
APPLICANT: SKETZA, ATNE; SCHMIGL, THOMAS
TITLE OF INVENTION: STREPTIDES WITH BINDING ACTIVITY FOR
TITLE OF INVENTION: STREPTAVIDIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
COUNTRY: USA
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
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0; Mismatches
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CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
PILLING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: 184,266
REFERENCE/DOCKET NUMBER: 34,266
REFERENCE/DOCKET NUMBER: 41,266
REFERENCE/DOCKET NUMBER: 41,266
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REFERENCE/DOCKET NUMBER: 41,266
REFERENCE/DOCKET NUMBER: 41,266
REGOURNIT CATALOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3832 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,675A
FILING DATE: 3-NOV-1993
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Best Local Similarity 99.8%;
Matches 1202; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: single
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US-08-148-675A-2
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US-08-148-675A-2
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PCT-US96-05611A-21/C
; Sequence 21, Application PC/TUS9605611A
; GENERAL INFORMATION:
; APPLICANT: Mueller, John P.
; APPLICANT: Lenardo. Michael J.
; APPLICANT: McFarland, Henry F.
; APPLICANT: Matis, Louis A.
; APPLICANT: Mueller, Eileen Elliott
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APPLICANT: Matis, Louis A.
APPLICANT: Mualler, Eileen Elliott
APPLICANT: No, Steven H.
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Wilkins, James C.
APPLICANT: Wilkins, James C.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: OF INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: ADDRESSE: Seth A. Fidel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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DESCRIPTION: PET Trc SO5/NI
DESCRIPTION: prokaryotic expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,208
FILING DATE: 02-MAY-1994
ATTONEY/AGENT INFORMATION:
NAME: Seth A. Fidel.
REGISTRATION NUMBER: 38,449
FERERENCE/DOCKET NUMBER: 38,449
TELECOMMUNICATION INFORMATION:
TELECHONE: (203)776-1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.3%; Score 1199.2; 99.8%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.4Mb storage
COMPUTER: Macintosh Cetris 610
                                                                                                                                                                                                                                                                   ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park (Alexion)
CITY: New Haven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (203)776-1790
TELEFAX: (203)772-3655
INFORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 5248 base paire
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Macintosh Cetris
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
CURRENT APPLICATION DATA:
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4510 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 4451
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                                                                                                                                                                                             TIGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA
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                                                                                                                    TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA
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US-10-263-103-35/c
; Sequence 35, Application US/10263103
; Patent No. 681723
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PASTEUR
; APPLICANT: Chevalier, Michel
; APPLICANT: El Habib, Raphaelle
; APPLICANT: Krell, Tino
; APPLICANT: Sodoyer, Regis
                                        361
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  APPLICANT: Myd. Stephen P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMBURICA M. Klee
CITY: Rairfield
STREET: 1951 Burr Street
CITY: Fairfield
STATE: COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: Other nucleic acid
DESCRIPTION: PET Trc SO5/NI
DESCRIPTION: prokaryotic expression vector
                                                                                                                                                                                                                                                                            CCMPUTER: MacINICOSHI CHILLES C. COMPUTER: MacINICOSHI CHILLES C. SOFTWARE: System 7
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05611A
FILING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
APPLICATION NUMBER: 30,399
REPERENE/DOCKET NUMBER: ALX-129
TELEFAX: (203) 255 1400
TELEFAX: (203) 255 1400
TELEFAX: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 21:
ENGTH: 5248 base pairs
TENDOMENSES: Double
TENDOMENSES: Double
TANDOMENSES: Double
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Best Local Simi:
Matches 1201;
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                                                            3782 TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGGATATCTCGGTAGTGGGATACG
                                                                                                                                       3722 ACGATACCGAAGACAGCTCATGTTATACCCGCCGTTAACCACCATCAAACAGGATTTTC
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                        TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG
                                                                                                     ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
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; Sequence 1, Application US/08929967
; Patent No. 5891637
; GENERAL INFORMATION:
; APPLICANT: RUppert, Siegfried J.W.
; TITLE OF INVENTION: Construction of Full-Length cDNA Libraries
; VORRESPONDENCE 3. 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genenech, Inc.
; STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Winfratin (Genentech)
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/929,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.3%; Score 1199.2;
99.8%; Pred. No. 0;
iive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger R. GINGER R. 33,055
REGISTRATION NUMBER: 31,055
TELECOMMUICATION INFORMATION:
TELEPHONE: 650/255-3216
TELEPHONE: 650/255-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 5443 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity 99.8
Matches 1201; Conservative
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TITLE OF INVENTION: gp41 antigen
FILE REFERENCE: 01-1692-A
CURRENT APPLICATION NUMBER: US/10/263,103
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 35
SOFFWARE: PatentIn version 3.1
SEQ ID NO 35
                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: plasmid pET-cer
US-10-263-103-35
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; CURRENT APPLICATION NUMBER: US/09/736,457 ; CURRENT FILING DATE: 2000-12-13 ; NUMBER OF SEQ ID NOS: 1864 ; SOPTWARE: PastSEQ for Windows Version 3.0 ; SEQ ID NO 785 ; LENGTH: 5502 ; TYPE: DNA ; ORGANISM: Homo sapien US-09-736-457-785	Query Match 36.3%; Score 1199.2; DB 4; Length 5502; Best Local Similarity 99.8%; Pred. No. 0; Matches 1201; Conservative 0; Mismatches 3; Indels 0; Gaps 0;	Qy         1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATGGCCCCGGAAGAGA 60	Qy 61 GICAATICAGGIGGIGGIGAATGIGAACCAGTAACGITATACGATGICGCAGAGIATGCCG 120	Oy 121 GIGTCTCTTATCACACCGTTTCCCCGCGTGGTGAACCAGCCCACCCTTTCTGCGAAAA 180	OY 181 CGCGGGAAAAGCGGCGGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240	Qy         241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACTCCAGTCTGGCCTGC         300           bb         4437 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGC         4378	Qy 301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360	Oy 361 TGGTGGTGTCGATGGTAGGAAGGGGGGGTGCGAAGCCTGTAAAGCGGGGGGTGCACAATC 420	Qy         421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA         480           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	QY         481         TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA         540           Db         4197         TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA         4138	QY         541         CACCCATGAGAGTATTATTTTCTCCCATGAGAGGAGCGACTGGGGGTGGAGCATC         600           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
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Job time : 357.4 secs
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                           3777 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
                                                                                                                                                                                CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT
                                                                                                                                                                                                  3597 CGCAAACCGCCTCTCCCCGGGGGGTTGGCATTAATGCAGCTGGCACGACAGGTTT
                                                                GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGGTGA
          ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
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JAPPLICANT: WAIG, TONGLONG
JAPPLICANT: Bangur, Chaitanya S.
JAPPLICANT: Bangur, Chaitanya S.
JAPPLICANT: Lodes, Michael A.
JAPPLICANT: Fanger, Gary
APPLICANT: Fanger, Tom
JAPPLICANT: Renger, Gary
APPLICANT: Rester, Marc
JAPPLICANT: Mannion, Jane
JITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
JITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
JITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
JITLE REFERENCE: 21012.4 7429
CURRENT APPLICATION NUMBER: US/09/614,124B
JURGER OF SEQ ID NOS: 1668
SOFTWARE: FaetSEQ for Windows Version 3.0
JENGTH: 5502
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36.3%; Score 1199.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1201; Conservative 0; Mismatches
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US-09-614-124B-785
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Sequence 18 from Patent WO0152620.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db\_xref="taxon:32630"
/note="Partial sequence of pMalZFPm4" DB 98.0%; Score 3232.8; 98.7%; Pred. No. 0; iive 0; Mismatches Conservative Query Match Best Local Similarity Matches 3258; Conserv 361 481 481 541 601 601 661 721 781 181 241 241 301 301 361 421 541 721 61 121 181 421 199 AUTHORS TITLE JOURNAL FEATURES

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160   TGGTGGTGTCGATGGTAGAACGAGCGGTCGAAGCCTGTAAAGCGGCGGTGCACAATC   420   1	661 CGCGTCTGCGTCTGGCTGGCATAATTATCTCACTCGCAATCAAATTCAGCCGATAG [	1021   AGGGGAATCAGCTGTTGCCCGTCTCATTGAAAAAAAAAA
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	AX202426 AX202426 AX202426 BDENTITION Sequence 14 from Patent W00152620. AX202436 AX202436 AX202436 AX202436 AX202426.1 GI:15392173 AX202	Query Match           Query Match         97.8%; Score 3226.4; DB 6; Length 3300;           Best Local Similarity         98.6%; Pred. No. 0;           Matches 3254; Conservative         0; Mismatches         46; Indels         0; Gaps           0y         1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATGGCCCGGAAGAGA         60           0y         61 GTCAATTCAGGTGGTGAAAACCTTTCGCGGTATGGCATGTGCCCGGAGGTATGCCG         120           0y         61 GTCAATTCAGGTGGTGAATGTGAAACCTATAACGTTATACGATGTCGCAGGTATGCCG         120           0y         61 GTCAATTCAGGTGGTGATGTGAAACCAGTAACCGTTATAACGATGTCGCAAGTATGCCG         120           0y         121 GTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGCAGCAGCTATTCTGCGAAAA         180           0y         121 GTGTCTTTATCAGACCGTTTCCCGCGTGGTGAACCAGCCAG

Db   2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580	2761 CCGGAATGTGGTAAGTCCTTCAGCCAGAGCAGCTCCCTGGTGCGCCACCAGCGTACCCAC		QY         3161         CAGGGTACCCACAGGGTGAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGC         3120           Db         3061         CAGGGTACCCACGGGTGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGC         3120           QY         3121         CAGCGCCCACCTGGAACGCCATCAACGACTCATACTGGCGAGAAGCCATACAAATGT         3180           Db         3121         CAGGCCGACCTGGAACGCCATCAACGACCATCATACTGGCGAGAAGCCATACAAATGT         3180	Qy         3181         CCAGAATGTGGCAAGTCTTTCTCAACTTCAGGCAACTTGGTCCGTCACCAACGTACTCAC         3240           Db         3181         CCAGAATGTGGCAAGTCTTTCTCTCGTCGTCACAATCTCGTCCGGCACCAACGTACTCAC         3240           Qy         3241         ACCGGTAAAAAACTAGTGGCCAGGCCGGCCAGTACCCGTACGACTTCCGGACTACGCT         3300           Db         3241         ACCGGTAAAAAACTAGTGGCCAGGCCAGTACCCGTACGACTTCCGGACTACGCT         3300	RESULT 4 AX202427 LOCUS DOCUS DEFINITION Sequence 15 from Patent WO0152620. ACCESSION AX202427 VERSION AX202427.1 GI:15392175 KEYWORDS SOURCE SOURCE ONGANISM synthetic construct ORGANISM sequences; artificial sequences.	AUTHORS AUTHOR
		1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCGATCGCTGTT 1860  1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCGATCGCTGTT 1860  1801 CCGTTTACCTGGGATGCCGTACGTTACAACGCCAACGCCGATTGCTTACCCGATCGCTGTT 1860  1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920  1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920  1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGGCAAACCCGCCAAAAACCTGAAAAGCGAACCCGCCAAAAACCTGAAAAGTAAAGAAAG				

ORIGIN	ZFPm2"	qa	GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
Query Best I Matche	Query Match 97.8%; Score 3226.4; DB 6; Length 3300; Best Local Similarity 98.6%; Pred. No. 0; Matches 3254; Conservative 0; Mismatches 46; Indels 0; Gaps 0;	ά d	AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCCAATA 
<i>&amp;</i> 8	1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCGGAAGAGA 60 	රු සි	1081 CGCAAACCGCCTCTCCCCGGCGTTGCATTCATTAATGCAGCTGGCACGACGTTT 1140
& A	16CCG 11111 16CCG	දු පු	1141 CCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA
දු පු		දු පු	GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGTGCACCCAATGCTTCTGGCG 
රු සි	181 CGCGGGAAAAAGTGGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240	දු පු	1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGTCGTAAATCACTGCATAATTCG 1320 
ර සි		දු පු	1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 1380 
& a	ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGGG 3	k d	1381 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAAATGTGTGGA 1440 
දු පු		දි සි	ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1 
λ d	421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCGGTGGATGACCAGGATGCCA 480 421 TTCTCGCGCAACGCGTCAATGGGGTCAATCATTAAATTAACTGTGGATGCCA 480	è 8	1501 GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGGAAG
8 & 8	TIGCTGTGGAAGCTGCCTGCACTAATGTTCGGCGTTATTCTTGAGGACGGCCGAAATTTGCTGGCGAAGCTGCCTGACCAGAATTTGTTGAAGCTGCCTGC	ò a	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGT 1620 
<i>≿</i> €	CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC	à a	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 
8 & 8	TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGTTTAGTTGGTCAATTGGGCGGCCCATTAAGTTCTGTCTCGGTTTTAGTGGGCGCCCATTAAGTTCTGTCTCGGTTTTAGTGGCGCCCATTAAGTTCTGTCTG	ò a	1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGGCTTTGGTGGCTAC 1740
ර සි	CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG	ò q	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800 1741 GCTCAATCTGGCCTGTTGGAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800
් ඊ සි	CGGAACGGGAAGGGACTGGCGTGTCCGGTTTTCACAAACCATGCAAAGGTGCTGA CGGAACGGGAAGGCGACTGGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA	ò a	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 
<i>≿</i> €	ATGAGGGCATCGTTCCCACTGCGATGGTTGCCAACGATCAGATGGGGCTGGGCGCAAAAAAAA	ò a	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 
8 & 8	TGGGGGCCATTACGAGTTCGGGGTGGCGGTTGGTGGGGGTATCTGGTTAGTGGGATACG	ò q	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGGCGCGCTGATGTTCAAC 1980 
<u>ک</u> خ		දු පු	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCTGAGGGGTTATGCGTTCAAG 2040
l è	GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAA	රු සි	2041 TATGAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100 

Qy         3181 CCAGAATGTGGCAAGTCTTTCTCAACTTCAGGCAACTTGGTCCGTCACGTACTCAC         3240           Db         3181 CCAGAATGTGGCAAGTCTTTCTCTCGGTCTGACAATCTCGTCCGGCACCAACGTACTCAC         3240           Qy         3241 ACCGGTAAAAAAATTGTCTGGCCGGCCCAGTACCCGTACGACTACCGACTACACACAC	RESULT 5 AX202428 LOCUS AX202428 LOCUS AX202428 DEFINITION Sequence 16 from Patent WO0152620. ACCESSION AX202428 VERSION AX202428 VERSION AX202428.1 GI:15392176 KEYWORDS	Σ	Patent: WO 0152620-A 16 26-JUL-2001; The Scripps Research Institute (US) ; SYNGENTA AGRICULTU DISCOVERY, INC. Location/Qualifiers e 1. 3300	/ Organization Synthetic Construct /mol type="unassigned DNA" /db_xref="taxon:32630" /note="PArtial sequence of pMa ZFPm3"	TIGAATGGTGCAAAACCTTTGGCGTATGGCATGATAGCGCCCGGAAGAGA	61 61		Oy 181 CGCGGGAAAAAGTGGAGGGGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240	OY 241 AACAACTGGCGGGAACAGTCGTTGCTGATTGCGTTGCCACTCCAGTCTGGCCCTGC 300	OY 301 ACGCGCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGGCCGATCAACTGGGTGCCAGCG 360	Oy 361 TGGTGGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGGGGGGG	QY 421 TTCTCGCGCAACGCGTCAGTGGGCTCATTAACTATCGGCTGGATGACCAGGATGCCA 480	Qy         481         TIGCIGIGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA         540           Db         481         TIGCTGTGGAAGCTGCACTAATGTTCCGGCGTTATTCTTGATGTCTCTGACCAGA         540
	2221 GCATGGTCCAACATCGACAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280  [	GGTCTG        GGTCTG GAAGAG	2401 GAAGGGGTTAATAAAGCAAACCGCTGGTGCCTTTTGTTTTTTTT			GGATCCTCTTCCTCTGTGGCCCAGGCGCCCTGAGCCCGGGGAGAAGCCCTATGCTTGT 	2/81 CCGGAATGTGGTAAGTCCTTCAGCCAGCAGCTGCCCCACCAGCGTACCCAC 2820 2/61 CCGGAATGTGGTAAGTCCTTCTCTAGAGCTCTCACCTGGTGCCCACCAGCGTACCAC 2820 2821 ACGGGTGAAAAACCGTATAAATGCCCAGAGGTGCGCCACCAGCGTAGAAAAACCGTAAAAAACCGTAAAAAACCGTAAAAAACCGTAAAAAAAA		rgrege ragaag		CGCCAC		

1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 	1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACGGCTTTGGTGGCTAC 1740	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800 	18 18	1861 GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCGGCCAAAAACCTGGGAA 1920 	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980 	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040	2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGGAAAGCG 2100 	2101 GGTCTGACCTTCCTGGTTGACCTCATTAAAAACAAACACATGAATGCAGACACCGATTAC 2160 	2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220 	2221 GCATGGTCCAACATCGACACCAGCAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280 	2281 AAGGGTCAACCATCCAAACCGTTCGTTGGGGGGGGGGGG	2341 CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA	2401 GAAGCGGTTAATAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACCAGGAAGAG 2460 	2461 TTGGCGAAAGATCCACGTATTGCCGCCACATGGAAAACGCCCAGAAAGGTGAAATCATG 2520 	2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580	2581 GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640 	2641 AACAACAACAACAATAACAATAACAACCCCGGGATCGAGGATTTCAGAATTC 2700 	GGATCCTCTTCCTCTGTGGCCCAGGCGCCCTCGAGCCCGGGGAGAAGCCCTATGCTTGT 276
\$ g	Qy Dp	S G	ος O	Qy Dp	oy Dp	oy B	Oy Dp	oy Dp	cy d	oy Oy	oy Oy	<u>ک</u> و	S G	ò q	SP GS	\$ B	ò 5	8 8
CACCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGGCGTGCAGCATC	CACCCATCAACAGTATTATTTTCCCCCATGAAGACGGTACGCGACTGGGGGGGG	661 CGCGTCTGCGTCTGGCTGGCATAAATGCTCGCGCTGCTCGCATTAAGTTCTGTCTCGG 860 661 CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCACCGGATAG 720 661 CGCGTCTGCGTCTGGCTGGCATAAATATTCTCACTCGCAATCAAATTCACTCGTAATAAATTCACTCGCAATCAAT	CGGAACGGGAAGGCGACTGGAGTGCCATTTCAACAACAACCATGCAATTGCAATTCAACAACGGAATGCTGAATTCAACAACGAAACGAATGCTGAATTTCAACAACAACAACAAATGCTGAATTTCAACAACAACAACAAACA		TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGATATCTCGGTAGTGGGATACG TGCGCGCCATTACCGAGTTCCGGCTTACTGGTGGGATATCTCGGTAGTGGGATACG TGCGCGCCATTACCGAGTTCCGGGCTTGGTGGGATATCTGGTAGTAGTAGTAGTAGTAGTAGTAGTAACG	ACGATACCGAAGACAGCTCATGTTATATCCGGCGTTAACCACCATCAAACAGGATTTTC 96	GCCTGCTGGGGCAAACCAGGGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGGGTGA 10	GCCTGCTGCTGCCGCCGCTGGCCCCTTGCTGCTGCTCTCTCTCTGGGGCCAGGCGGTGA 102 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAAAAA	GGCAAACCGCCTCTCCCCGGTTGCCCGATTCATTAATGCACCCTGGCGCCCGTTT 114 CGCAAACCGCCTCTCCCCGCGCGTTGCCGATTCATTAATGCAGCTGGCACGACGAGTTT 114 CCG131ACCTCTCTCCCCCCCCCCCCTTTTTT 114	CCCGACTGGAAAGCGGGCAGTGGCCGATTCATTAATGCAGCTGGCACACATTATATTACTGCAGTTGAACGCGCATTAGTTAG	CCCGALIGGRANGCGGGGCGCARGCGCAAIIAAIGIGGGGITAGCICACICAIIAG IZ GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGGGCACCAATGCTTCTGGCG 12	GCACAATICICAIGITICACAGCITALCATCGACIGCACCCAATGCITCIGGCG 128 TCAGGCAGCCATCGGAAGCTGTGGTATGCCTGTGCAGGTCGTAAATCACTGCATAATTCG 132 TCAGGCAGCCATCGGAAGCTGTGCTATGCCTGTGCAAATCACTGCATAATTCG 132 TCTAGACTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TCAGGCCAGCCATCGGAAGCCGTGGTGGCAGGTCGTAAATCACTGCATAAATCGGTTGAGTTCGGTGAGTCGGTTGAGTTGGTGTTTTTTGGGCGCGACATCATAACGGTTTTTAGGGCGCGACATCATAACGGTTTTTTTT	CTGGCAAATATTCTGAAATGAGCTGTTGAATATTAATCATCGGCCGGAATAATGTGTGGGT 138	CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTGTGATGTGTGTG	ATTGTGASCGGGTAACAATTTCACACAGGAAACAGCCAGTCGGTTTAGGTGTTTTCACGA 1 GCACTTCACCAACAAGGACCATAGAATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG 1	1501 GCACTICACCAACAAGGACCAIAGATIATGAAAACTIGAAGAAGGIAAACTIGGIAATCIGG 1550 1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTGGGTAAGAAATTCGAGAAAGAT 1620	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT 1620

AKEFLENYILITDEGILEAVNEDKPLGAVALKSYEEELAKDPRIAATHENAQKGEIMPNI PQMSARWYANTAVINAASGRQTVDEALKDAQTNSSSNNNNNNNNNNLGIEGRISEFG SSSPGKPPRLVGGPMDASYBEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIV AGVNYFLDVELGRTTCTKTQPNDDNCPFHDPDHLKRAFCESQIYAVPWGTWTLSK TCODASASHHHHHGGERTTCTKTQRTQKRKKKSFCSGRQTYALLSK TCODASASHHHHHGGETRQAKKKKRKRAFCSGYGYNDWIVATAPEPGYH AFYCHGECPFPLADHLNSTNHAIVQTLVNSVNSKIPKACCVPTELSAISMLYLDENEK VLIKNYQDMVVEGCGCR"  misc_feature	Query Match         82.0%;         Score 2705.8;         DB 6;         Length 7373;           Best Local Similarity 99.2%;         Pred. No. 0;         DB 6;         Length 7373;           Matches 2719;         Conservative 0;         Mismatches 22;         Indels 0;         Gaps 0;           Qy         1 CCGACACCATCGAATGGTGAAAACTTTCGCGGTATGGCATGATAAGGCCCGGAAGAGA 60         Db 1 CCGACACCACGAATGGTGAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60         CGGACACCATGAATGTGAAAACCATAAACGTAATGCGATGAATGTGCGAAGATGTGCC         120           Db         61 GTCAATTCAGGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTTGCCC         120         Db 61 GTCAATTCAGGGTGAAATGTGAAACCAGTAACGATAATACGAATGTCGCAGAGTTATACCAATGTCGCAGAGTTATACCAATGCCCAGAGTTAATGCCG 120         120	121 GTGTCTTATCAGACCGTTTCCCGCGTGGTGACCAGGCCACGTTTCTGCGAAAA 180   121 GTGTCTTTATCAGACCAGTTTCCGCGAAAA 180   181 GTGTCTTTTCTGGAAAAA 180   181 GTGTCTTTTTCTGGAAAAA 180   181 CGCGGAAAAAAGTGGAAGCGGTGGCGGGGCGAGCCAGGTTTCTGCGAAAA 180   181 CGCGGGAAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240   181 CGCGGGAAAAAAGTGGAAGCGGCGATGGCGAGCTGAATTACATTCCCAACCGCTGGCAC 240   181 CGCGGGAAAAAAGTGGAAACGGCGATGCTGAATTACATTCCCAACCGCTGGCAC 300   241 AACAACTGGCGGAAACGCTTGCTGATTGCGATTGCCACTCCAGTCTGGCCTGC 300   241 AACAACTGGCGGAAACAGTCGTTGCTGATTGCCGTTGCCAGTCTGGCCTGC 300   241 AACAACTGGCGGCAAAAATGTCGGGGGAATTAAATCTCGGCGCCACTCAGTCTGGCCTGC 300   241 AACAACTGGCGGCAAAATTGTCGCGAATTAAATCTCGGCGCCACCACTCAGTCCTGGCCAGCG 360   241 AACAACTGGCGCAAAATTGTCGCGAATTAAATCTCGGCGCCACCACTCAGTCTGGCCCAGCG 360   241 AACAACTGGCGCAAAATTGTCGCGAATTAAAATCTCGCGCCCAATCAACTGGCCCAGCG 360   261	301 361 361 421 481 681 541 601 601	Oy 721 CGGAACGGCAACTGCAGTGCCATGTCCGGTTTTCAACAAACCATGCTGA 780
	AGAAG AGAAG AGAAG SACAC GCCAC TTAGC	3121 3121 3181 3181 3241	44  TION Sequence 1  ION AX284144  NAX284144  NS synthetic synthetic sequence 1  NCE 1  NAE Patent sequence NAE Patent with Patent sequence NAE NAE NAE NAE NAE NAE NAE NAE NAE NAE	/protein_id="CAD12160.1" //db_xaref="dal1044813" //db_xaref="dal1044813" //translation="MKIEBERGEKUVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKL EEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAPQDKLYPFTWDAVRYNG KLIAVPIAVEALSLIYNKDLLPNPFKTWEET PALDKELKAKKKSALMFNLOBFYFWP LIAADCGYARFKRENGKYDI PROVGVDNAGARAGLTFLYDLIKNKHMNADTDYSIAEAAF NKGETAMTINGPWAWSNIDTSKVNYGVTVLPFKGQPSKFPVGVLSAGINAASPNKEL

Oy 1921 GAGATCCCGGCGCTGGATAAGAACTGAAAGCGAAAGGTAAGGCGCTGATGTTCAAC 1980  1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGTGATTCAAC 1980  Oy 1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTTCAAC 1980  Oy 1981 CTGCAAGAACCGTACTTCACCTGGTGATTGCTGCTGACGGGGTTATGCGTTCAAG 2040  Db 1981 CTGCAAGAACCGCAACTTCACCTGATGCTGATGCTGACGGGGTTATGCGTTCAAG 2040  Oy 2041 TATGAAAACGGCAAGTACACTTAAAAACGGGGGGAAAACGGTGGGGGGAAAGCG 2100  2041 TATGAAAACGGCAAGTACACTTAAAAACGGCGGGAAAACGCTGGCGCGAAAACG 2100		Db   2221	Oy 2401 GAAGCGGTTAATAAACACCGCTGGGTGCCGTAGCGCTGAAGTCTTACCAGGAAGAG 2460  Db 2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACCAGGAAGAG 2460  Oy 2461 TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCAGAAAGTGAAATCATG 2520  Db 2461 TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGTGAAATCATG 2520  Oy 2521 CCGAACATCCCGCAAAGATCTCCGGTTTCTGGTACTGGAAAAGGTGAAATCATG 2520	Db   2521	CTTCCTCTGGCCCAGGCGG 	ITION Sequence 5 from Patent W00144467.  SION AX172306.  AX172306.1 GI:14597487  Substantic construct  ANISM synthetic construct  ANISM synthetic construct  Cher sequences; artificial sequences.  ENCE I obtaining human cdc25 phosphatases a identifying human cdc25 phosphatases a identifying human cdc25 phosphatases a identifying human cdc25 phosphatase modulators  RNAL PATENTE DE CONSEILS DE RECHERCHES ET D'APPLICAT
TGCGCGCCATTACCGAGTCCGGGCTGGGGTGGGGGATATCTCGGTAGTGGGATACG	GCCTGCTGGGGCAAACCAGGGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGGGGGTGAACGGCTGAACTCTCTCAGGGCCAGGGGGGGTGAAACGAAACAACACCCTTGCTGACCCAATAAGGAAAACAACCACCTTGGCGCCCAATAAGGCAATCACTCAC	141   CCCGACTGGAAGCGGCAACGCAATTAATGTGACTTAGTTAG	TGTCGCTCAAGGCGCACTCCCGTTCTGGATATGTTTTTTGCGCCGACATCATAACGGTT TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTTGCGCCGACATCATAACGGTT TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTTGCGCCGACATCATAACGGTT CTGGCAAATATTCTGAAATGAGCTGTTAACAATTAATCATCGGCTCGTATAATGTGGGAT CTGGCAAATATTCTGAAATGAGCTGTTAACAATTAATCATCGGCTCGTATAATGTGGGA		ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGGAA	CTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT   CTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT   CTCAATCTGGCCTGTTGGAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT   CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTACCTGGGATGCCTTACCCGGATGCTTACCCGGTTTACCTGGTTTACCTGGTTACCCGGATGGCTTTACGGGCAAGCTGTTTATAACAAAGGCTGATGCTTACCCGGCAAAAACCTGGGAA   CAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGGCGGAACCCGGCAAAAACCTGGGAA   CAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGGCAAAAACCTGGGAA

/note="Plasmid pMAL-c2x"	Query Match 81.8%; Score 2701; DB 6; Length 6648; Best Local Similarity 99.8%; Pred. No. 0; Matches 2704; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	Oy 1 CCGACACCATGGAATGGTGCAAAACCTTTCGCGGTATGGCATGGTAGCGCCCGGAAGAGA 60	Qy         6.1 GTCAATTCAGGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG         1.20           Db         6.1 GTCAATTCAGGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG         1.20	Oy 121 GTGTCTTATCAGACCGTTTCCCGGTGGTGAACCAGGCCAGCCA	Oy 181 CGCGGGAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240	QY         241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC         300           Db         241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCCAGTCTGGCCGTG         300	Oy 301 ACGCCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCCGATCAACTGGGTGCCAGCG 360	Oy 361 TGGTGGTGTGGAAGGAAGGGGGGGTCGAAGCGGGGGGGGG	Oy 421 TICTCGGGAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 480	Oy 481 TIGCTGIGGAAGCTGCCTGCACTAATGTICCGGCGTTATTTCTTGATGTCTCTGACCAGA 540	Oy 541 CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGGGGCTGGAGCATC 600	Oy 601 TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 660	Qy         661 CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAT	QY         781 ATGAGGCATCGTTCCCACTGCGATGCTTGCCAACGATCAGATGCGCTGGCCGCAA 840           DD         781 ATGAGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA 840	841 TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGGGGATATCTCGGTAGTGGGATACG	DB 84.1 TOCGCCCATTACCGAGTCCGGGCTCGCTCGGTGATCTCCGGTAGTGGGGATACC 900 Qy 901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACACCACCATCAACAGGGTTTTC 960	901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC	Oy 961 GCTGCTGGGGAAACCAGCGTGGACGGCTTGCTGCAACTCTCAGGGCCAGGCGGTGA 1020
	OY 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGGTGGATAACGCTGGCGCGAAAGCG 2100 	OY 2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAACAACAAGAAGAGACACGATTAC 2160	OY 2161 TCCATGGCAGAAGCTGCCTTTAATAAAGGGAAACAGGGATGACCATCAAGGGCCGTGG 2220	OY 2221 GCATGGTCCAACATCGACACGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280	QY         2281 AAGGGTCAACCATCCAAACCGTTCGTTGGCGGCGGGGGGGG	OY 2341 CCGAACAAAGAGCTGGCAAAGATTCCTCGAAAACTATCTGCTGACTGA	QY 2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG 2460	Qy 2461 TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAACGCCCAGAAAGGTGAAATCATG 2520	OY 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTG	OY 2581 GCCAGGGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGGGCAGACTAATTCGAGCTCG 2640	OY 2641 AACAACAACAACAATAACAATAACAACCTCGGGATCGAGGGAAGGATTTCAGAATTC 2700	Oy 2701 GGATCCTCT 2709  Db 2701 GGATCCTCT 2709	RESULT 8 AX377531 AX377531 AX377531 AX377531 DEFINITION Sequence 8 from Patent W00212553. ACCESSION AX377531 VERSION AX377531. GI:19573717	ALINOUS SYNTHETIC CONSTRUCT ORGANISM SYNTHETIC CONSTRUCT ORGANISM SYNTHETIC CONSTRUCT OTHER SEQUENCES; ARTIFICIAL SEQUENCES.	ANTHORS Kappel, A., Polakowski, T., Pignot, M., Windhab, N., Behrensdorf, H. and Muth, J. TITE Mathod for descript matrices is analyzed to consider	ı,	FEATURES Location/Qualifiers Source 16648	/organism="bynthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630"

	OY 2281 AAGGGTCAACCATCCAAACCGTTCGTGGGCGCAGGTATTAACGCCGCCAGT 2340  DD 2281 AAGGGTCAACCATCCAAACCGTTCGTTGGCGCGCAGGTATTAACGCCGCCAGT 2340  C2341 CCGAACAAAGGGTGGCAAAAGGTTCCTCGAAAACTATCTGCTGACTGA	Oy 2461 TTGGGGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520  2461 TTGGCGAAAAGATCCACGTATTGCCGCCACTATGGAAAACGCCCAGAAAGGTGAAATCATG 2520  Qy 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580  Db 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580  Oy 2581 GCCAGCGGTGTCTGCTGTTCTGGTATGCCGTGCTACTGCGGTGATCAACGCC 2580  Db 2581 GCCAGCGGTGTCTGCAGATGCCGTGCGTACTTCGGGTGATCAACGCC 2580  Db 2581 GCCAGCGGTGCTGCAATGAAGCCCTCAAAAGACGCGCAGACTTATTCGAGCTCG 2640	Qy         2641 AACAACAACAACAACAATAACAACAACAACCTCGGGATCGAGGAATTTCAGAATTC 2700           Db         2641 AACAACAACAACAATAACAATAACAACACCTCGGGATCGAGGGAAGGATTTCAGAATTC 2700           Qy         2701 GGATCCTCT 2709           Db         2701 GGATCCTCT 2709		REFERENCE 1 (bases 1 to 7475)  AUTHORS Attwood,M.R. and HUSEL,D.N.  TITLE ANTIVIRAL PEPTIDE DERIVATIVES  JOURNAL PATENT: WO 9822496-A 1 28-MAY-1998;  HOFFMANN IA ROCHE (CH)  FEATURES Location/Qualifiers  1. 7475  /mol_type="unassigned DNA"  /db_xref="taxon:32644"	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 2700; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CCGACACCATGGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60
961 GCCTGCTGGGGCAAACCAGCGTGGACCGCAACTCTCTCAGGGCCAGGCGGTGA 1020   1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTAAAAAAAAA	GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGCGACCCATGTCTCTCTC	CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGCCCCGTATAATGTGTGGA 14 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 14 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 14 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 15 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 15 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 15 GCACTTCACCAACAAGAACAGAAACAGAAGAAGAGGTAAACTGGTAATCTGG 15		GCGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGCCTTTGGTGGCTAC [	1861 GAAGGTTATCCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860  1861 GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCCGCAAAACCTGGGAA 1920  1861 GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920  1921 GAAGCGTTATCGCTGGATAAAGAACTGAAAGGTACGCAACGCCCAAAAACCTGGGAA 1920  1921 GAAGCGTTGTTTATAAACAAAAGAACTGAAAGGTAAGAAGCGCGTGATGTTCAAC 1980  1921 GAAGCGTGGATAAAGAACTGAAAGGGAAAGGTAAGAGGCGCTGATGTTCAAC 1980  1981 CTGCAAGAACCCTACTCACCTGGCGCTGAATGCTTCAACGGGGGGTTATGCGTTCAAG 2040	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCGGGGGTTATGCGTTCAAG 2040 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGGAAAGCG 2100 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100

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Oy 2521 CCGAACACCTCTCTTCTCTTCTCTCTCTCTCCTCCTCCTCCTC	11 94 TION ION N	SOURCE SOURCE UNKnown. ORGANISM Unknown. Unclassified. Unclassified.  AUTHORS Attwood,M.Richard., Hurst,D.Nigel., Jones,P.Stephen., Kay,P.Brittain., Raynham,T.Michael. and Wilson,F.Xavier. TITLE Antiviral medicaments JOURNAL Patent: US 6372883-A 116-ARR-2002; FEATURES Location/Qualifiers Source /organism=unknown. /mol tyne="unknown"	ORIGIN  Query Match  81.8%; Score 2700; DB 6; Length 7475;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 2700; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 CCGACACCATGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGGCCCCGGAAGAG 60  Db 1 CCGACACCATCGAATGGTGCAAAACCTTTTCGCGGTATGGCATGATAGCCCCCGGAAGAGA 60	Qy	181 GGGGGAAAAAGAGGGGGATGGCGAGGTGAATTACATTCCCAACCGGGTGGCAC 181 GGGGGAAAAAGAGGGGGATGGCGAAGCTGAATTACATTCCCAACCGGTGGGAC 181 GGGGGAAAAAGAGGGGTTGGCGAAGTGAATTACATTCCCAACCGGTGGGAC 241 AACAACTGGCGGCAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGC 241 AACAACTGGCGGGAAAAAAAAGTGGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGC 241 AACAACTGGCGGGCAAAAAAGTGGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGCTAGTCTTGCTAGTCTTGCTAGTCTTGCTAGTCTTGCTAGTCTTGCTAGTCTTGCTAGTCTTGCTTG	Qy         301 ACGCGCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG         360           bb         301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG         360           Qy         361 TGGTGGTGTCGATGAAACGAAGCGGCGTCGAAGCCTGTAAAGCGGGGGTGCACAATC         420           Db         361 TGGTGGTGTCGATGGTAGAACGGCGTCGAAGCCTGTAAAGCGGGGGTGCACAATC         420
1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT   1380	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT 1800	GAGATCCCGGCGCTGGATAAGAACTGAAAGCGAAAGGTAAGGCGCGCTGATGTTCAAC [	2041 TATGAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100	2161 TCCATCGCAGAAGCTGCCTTTAATAAAGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220	2281 AAGGGTCAACCATCCAAACCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT 2340

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QY         421         TTCTCGCGAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA         480           Db         421         TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA         480           QY         481         TTGCTGTGGAACGCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA         540           Db         481         TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTTTGATGTCTTGACAGA         540           QY         541         CACCCATCAACAGTATTATTTTCTCCCATGAAGAGCGACCAGGAGCATC         600           S41         CACCCATCAACAGTATTATTTTCTCCCATGAAGACGATACGACTTCGACCATCAACAGTATTTTTTCTCCCATGAACAGTATTTTTTCTCCCATGAACAGTATTTTTTCTCCCATGAACAGTATTTTTTCTCCCATGAACAGTATTTTTTTT	TOGTCGCATTGGGTCACCAGCAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTG	661 CGCGTCTGCTGCTGGCTGGCTAAATTCTCGCTATTCTGCTGTTTTTTTT	781 ATGAGGGATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGGCGCAA 840	ACGATACCGAAGACGCTCATGTTATCCCGCCGTTAACCGACGTCAACAGGATTTTC ACGATACCGAAGACAGCTCATGTTATTATCCCGCCGTTAACCACCATCAAACAGGATTTTTC ACGATACCGAAGACAGCTCATGTTATTATCCCGCCGTTAACCACCATCAAACAGGATTTTTTC	901 GCCTGCTGGGGGGGGGGGTTGCTGCAGCTGCTGCAGGGCCAGGCGGGGG 1020 961 GCCTGCTGGGGGACGGTTGCTTGCTGCTGCTGCTGCGGCCAGGCGGGGGTGA 1020 961 GCCTGCTGGGGAACCAGGGTGGGACGCTTGCTGCAGGCCTGGGGGGGTGA 1020 1021 AGGGCAATCAGCTGCTGCTGGTGAAAAGAAAACCACCTGGGGGCCCAATA 1080 1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAACCACCTGGCGCCCAATA 1080 1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAACCACCTGGCGCCCAATA 1080	CAPACCGCCTCTCCCCGCGGTTGGCCGATTCATTAATGCAGCTGGCACGACGACGACGGTTTTAATGCAGCTGGCACGACGACGACGACGACGACGACGACGACGACGACGA	1141 CCCGACTGGAAGCGGCAGTGACCCAATTAATGTGAGTTAGTT	1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320 	GCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 	1391 CIGGCAATATICIGAATIGACIGITGACAATAATGATCACCCCGCTGATAATGAGGA 1440 1381 CIGGCAATATICIGAAATGAGCTGTTGACAATTAATCATCGCTCGTATAATGTGGA 1440 1441 ATTGTGAGCGGATAACAATTCACACAGGAAACAGCCAGTCCGTTTAAGGTGTTTTCACGA 1500 1441 ATTGTGAGCGGATAACAATTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 1441 ATTGTGAGCGGATAACAATTCACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500

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	QY         2641 AACAACAACAATAACAATAACAACAACCTCGGGATCGAGGAAGGA	RESULT 12 AX377532 LOCUS DEFINITION Sequence 9 from Patent WO0212553. ACESSION AX377532 VERSION AX377532.1 GI:19573718		AUTHORS Kappel.A., Polakowski,T., Pignot,M., Windhab,N., Behrensdorf,H. and Muth,J. TITLE Method for detecting mutations in nucleotide sequences	e e	/ Anol type="unastgned DNA" / Ab xref="taxon:32630" / noTe="pMALc2x-mutS Plasmid"	Query Match 81.8%; Score 2698; DB 6; Length 9191; Best Local Similarity 99.8%; Pred. No. 0; Matches 2701; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	SCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAA 60	GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG		CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACCCGCGTGGCACGCCGGGAATTACATTCCAACCGCGTGGCGATGGCGGAGCTGAATTACATTCCAACCGCGTGGCGATGGCGGAGCTGAATTACATTCCAACCGCGTGGAATACATTCCAACCGCGTGGCATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCA		301 ACGCGCGTCGCAAATTGTCGCGGCGATTAAATCTCGGCCGATCAACTGGGTGCCAGCG 	361 TGGTGGTGTCGATGGTAGAACGAGGGGGGTCGAAGCCTGTAAAGCGGGGGGGG	421 TTCTCGCGCAACGCGTCAGTCATTAACTATCCGCTGGATGACCAGGATGCCA 421 TTCTCGCCGAACGCGTCAGTCATTAACTATCCGCTGGATGACCAGGATGCCA 421 TTCTCGCCGAACGCGTCGCTCCATCATCATCACTACAACGATGACCAACAACAACAACAACAACAACAACAACAACAACAAC	481 TIGCTGTGGAAGCTGCCACATAATGTTCCGGCGTTATTTCTTGATGTCTCACCAGA	DD 481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGGCGTTATTTCTTGATGTCTCTGACCAGA 540 Qy 541 CACCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGGGGGGGCGTGGGGCATG 600

1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT 1680

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AF097412 6724 bp DNA circular SYN 28-JAN-2002
Expression vector pMBP-parallell, complete sequence.
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                                                                                                                                                                                                                                                                                                                             Expression vector pWBP-parallell other sequences; artificial sequences; vectors.

(bases 1 to 6724)
Sheffield, P., Garrard, S. and Derewenda, Z.
Overcoming expression and purification problems of RhoGDI using a family of 'parallel' expression vectors
Protein Expr. Purif. 15 (1), 34-39 (1999)
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Sheffield, P.J., Garrard, S.M. and Derewenda, Z.S.
Sheffield, P.J., Garrard, S.M. and Derewenda, Z.S.
Submission
Submitted (05-007-1998) Molecular Physiology and Biological
Physics, University of Virginia, 4215 Jordan Hall, 1300 Jefferson
Park Avenue, Charlottesville, Virginia 22908, USA
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LKSALPAGWFIADKSGAGERGSRGIIAALGEGLITLASRQQLIDWMEADKVAGPL
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Yan, R., Tomasselli, A.G., Gurney, M.E., Emmons, T.L., Bienkowski, M.J. and Heinrikson, R.L. Substrates and assays for  $\_g(b)$ -secretase activity

REFERENCE AUTHORS

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/mol\_type="unassigned DNA"
Mol\_xref="taxon:32644"
/note="fusion protein comprising with 125 amino" Patent: WO 0206306-A 194 24-JAN-2002; PHARWACIA & UPJOHN COMPANY (US) Location/Qualifiers 1. .6806 79.9%; Score 2636.8; llarity 99.9%; Pred. No. 0; Conservative 0; Mismatches 781 781 841 ☆ qq ò

1981 CTGCAAGAACCGTACTTCACCTGGCCGTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2010   1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2010   2011 TATGAAAACGGCACGCACTTAAAAACGCGCGCGCGGGGGGCGGAAGCG 2100   2011 TATGAAAACGGCACACCACTTAAAAACGCGGCGCGGGGGCGGGAAGCG 2100   2011 TATGAAAACGGCACACACACACACACACACACACACACAC	RESULT 15 AP031088 LOCUS DEPINITION SHULLE VECTOR DWAL-DIII, Complete sequence. ACCESSION VERSION AP031088 VERSION AP031088 VERSION AP031088.1 GI:2623821 KEYWORDS SOURCE SOURCE ORGANISM AP031088.1 GI:2623821 KEYWORDS SOURCE SOURCE ORGANISM AP031088.1 GI:2623821 KEYWORDS SOURCE ORGANISM AP031088.1 GI:2623821 CREFERENCE I Chasses 1 to 6706 AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS DEPINE POD381 PUBMED 77 Barbas.CF: III, Noren,C.J. TITLE POD4104 Anal. Biochem. 264 (1), 87-97 (1998) MEDLINE PUBMED 77 Barbas.CF: Organisan JOURNAL Anal. Biochem. 264 (1), 87-97 (1998) MEDLINE PUBMED 77 Barbas.CF: Organisan JOURNAL Anal. Biochem. 264 (1), 87-97 (1998) MEDLINE PUBMED 77 Barbas.CF: Organisan JOURNAL ANAL. Biochem. 264 (1), 87-97 (1998) MEDLINE PUBMED 77 Barbas.CF: Organisan JOURNAL ANAL. Biochem. 264 (1), 87-97 (1998) MEDLINE PUBMED 77 Barbas.CF: Organisan JOURNAL Beverly, MA 01915, USA FEATURES 1. 6706  //mol_type="genomic DNA"
10   ACGATACCGARGACAGCTATTATATCCGGCGATAACCACCATCAACAGGATTTC   900   ACGATACCGAAGACACTATATATCCGGCGGTAACCACCATCAACAGGATTTC   960   901   ACGATACCGAAGACACTATATATCCGGCGGTAACCACCATCAACAGGATTTTC   960   961   GCCTGCTGGGGGAACACCAGGCGTAATATCCCGGCGGTAACCAGGATTTTC   960   961   GCCTGCTGGGGGCAACACCAGGCGTAACCAGGCGTAACCAGGATTTTC   960   961   GCCTGCTGGGGCAACACCAGGCGTAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTGAACCAGGCGTTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1561 ATTAACGGCGATAAAGGCTATAACGGTCCGCTGAAGTCGGTAAGAAATTCGAGAAAGGT   1620   11   1   1   1   1   1   1   1   1

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                                                                                                                                                                                                             /gene="lac1"
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1528. .2976
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Zinc finger protein; ZFP; gene expression; metabolic pathway regulator; modulation; plant technology; agriculture; Ap3; APETALA3; ds.
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/*tag b
Dound moiety= "F1-f2 primer"
2770. 2850
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824. .2889
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product= "ZFPAp3 protein"
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

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"F2-f primer"

"F2-b primer"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target nucleotide sequence, where the expression of the target gene in the plant cells is modulated. The ZFP and fusions of the ZFP proteins are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the target gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-Ap3 (APETALA3) and ZFPAp3 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATGAGGGCCCGGAAGAGA
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21-JUL-2000; 2000US-00620897.
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P-PSDB; AAE06005.
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1080 1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG 1260 240 480 CGCGGGAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360 420 480 540 540 900 9 099 720 720 780 780 840 840 900 900 960 960 CGCGGGAAAAAGTGGAGGGGGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC TICTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCCATTAAGTTCTGTCTCGG CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGGATAG TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTTCTTGATGTCTCTGACCAGA TIGCTGTGGAAGCTGCCTGCACTAATGTTCCGGGCGTTATTTCTTGATGTCTGACCAGA CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGACATC CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCAAGCAAATGCTGA CCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTAG TGGTGGTGTCGATGGTAGAACGAAGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATC TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCCATTAAGTTCTGTCTCGG CGCGTCTGCGTCTGGCTGGCTTGCATAATATCTCACTCGCAATCAAATTCAGCCGATAG ATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA ATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG 841 rececentraceastreceserrececerrecesarraceararecesarrace 1081 CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACGGTTT GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCC 961 GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCCAATA CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT 901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGT

2341 2401 2401	2461 TIGGCGAAGATCCAGGTATTGCCGCCACCATGGAAAGGCCCAGAAAGGTGAAATCATG		2641	2701	2761	2821	2881	2941 2941	3001	3061	3121	3181	3241 ACGGTAAAAACTAGTGGCCAGGCCGCCAGTACCCGTAGCGTGCCGGACTTCCGGACTAGCT 3241 ACCGGTAAAAAACTAGTGGCCAGGCCGGCCAGTACCGTACGACGTTCCGGACTTCCGGACTACGCT	SULT 2 D11591 AAD11591 standard, DNA, 3300 BP.		Partial sequence of pMal-m4 and ZFPm4 DNA.
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1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320	1381   CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440 	1441 ATTGTGAGGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 1501 GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG 1560 1501 GCACTTCACCAACAAGGACCATAGATATGAAAACTGAAAAAGGTAAACTGGTAATCTGG 1560	ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 	1681 GCGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTAC 1740 	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800 	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 	1861 GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980 	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCTGGGGGGGTTATGCGTTCAAG 2040 	TATGAAACGCCAAGTACGACATTAAACACGTGGGCGTGGATAACGCTGGCGCGAAAGCGTTAAACACGCTGGCGCGAAAGCGTGAAAACGCTGGCGCGAAAGCGTGGACGTGGGCGTGGAAAACGCCTGGCGCGAAAGCG		2161 TCCATCGCAGAAGCTGCCTTTAATAAGGCGAAACAGCGATGACCATCAACGGCCCGGTGG 2220 	2221 GCATGGTCCAACATCGACAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280 	AAGGGTCAACCATCCAAACCGTTCGTTGGTGCTGAGCGCAGGTATTAACGCCGCCAGT 	2341 CCGAACAAAGGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA

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New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant ceils a disorder that is associated with abnormal expression of the
Zinc finger protein; ZFP; gene expression; metabolic pathway regulator; modulation; plant technology; agriculture; ds.
                                                                                                                    product= "ZPPm4 protein"
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bound moiety= "F2-b primer"
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916. 72973
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                    The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) Which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZPP binding to the target cells within a target gene and allowing the ZPP binding to the target cells is modulated. The ZPP and fusions of the ZPP proteins are useful cor modulating or regulating gene expression of the target gene in the plant for modulating or regulating agene expression and metabolic pathways in agricultural technology. The method is useful particularly for treating a gricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with partial sequence of pMal-m4 and ZPPm4 bNA
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Best Local Similarity 98.7%; Pred. No. 0;
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1912 GARACCTIVATOCTRACTARATA AND ACCIDANA CONTRACTOR COCCOCCANANIC COCCOCCANANIC CONTRACTOR AND ACCIDANA CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC CONTRACTOR COCCOCCANANIC COCCOCCANANIC CONTRACTOR COCCOCCANANIC COCCOCCANAIC COCCOCCANAIC C
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Best Local Similarity 98.6
Matches 3254; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      3241 ACCGGTAAAAAAACTAGTGGCCAGGCCAGTACCCGTACGACGTTCCGGACTACGCT 3300
                                                   CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCAGCACCAGTGGCTCCTTGGTTAGACAC 3060
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                                                                                                                                        CAGCGTACCCACACGGTGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGC
                                                                                                                                                                       3061 CAGCGTACCCACACGGTGAAAAACCGTATAAATGCCCAGAGTGCGGGAAATCTTTTAGC
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                                                                                              CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCTCTCAGAGCTCTCAGCTGCGCCAC
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. .3225, aa:Ser)
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/bound_moiety= "F1-f1 primer"
2824. .2889
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bound_moiety= "F1-f2 primer"
1770. .2850
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (EFP) Which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZPP binding to the target gene within a target gene and allowing the ZPP binding to the target cells is modulated. The ZPP and fusions of the ZPP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZPP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-m1 and ZPPm1 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New zinc finger proteins, useful for modulating or regulating gene
expression and metabolic pathways in plants, e.g. for treating in the
plant cells a disorder that is associated with abnormal expression of the
target gene.
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'bound_moiety= "F6-b2 primer"
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bound moiety= "F2-b primer"
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/bound_moiety= "F2-f primer"
2916. .2973
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168. 3225
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/bound_moiety= "F3-b1
/953. .3021
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC.
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2992. .3042
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97.8%; Score 3226.4; 98.6%; Pred. No. 0; live 0; Mismatches

DB 4; Length 3300;

	TGTGGCAAATATTCTGAAATGAGCTGTTGGATAATGTTTTTTGCGCCGACATCATAACGGTT CTGGCAAATATTCTGAAATGAGCTGTTGGAATAATGTTTTTTGCGCCGACATCATAATGGTT CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA ATTGTGAACGGATAACAATTTCACACAGGAAACAGCCACTCTTAGGTGTTTTCACGA ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA GCACTTCACCCAACAAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA GCACTTCACCCAACAAGATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA GCACTTCACCCAACAAAGATTATGAAAAACTGAAAAACTGGTAATCTGG	ATTAACGCCATTAAGGCTATAACGTCCCTGAAGTAGGTAAGAATTCGAGAAAGATTAACGCCATTAAAGGCTATTCGCTGAAGTTCGTGAAGATTCGAGAAAGATTAACGCCATTAAAGGCTTTCGCTGCTGCTGAAGTTCGTTAAAGATTCGAGAAAGATTCCCACAGGATTAACGGCAATTAAAGTCCCTTGAGCATCCGAATAAACTGGAAGAAATTCCCACAGGTTACCGAATTAAAGTTCCCGTTGAGCATCCGAATAAACTGGAAGAAATTCCCACAGGTTACCGAATTAAAGTTCCCATGAGATTCCCACAGGTTGCCGAAATTAAAGTTCCATGAGAATTCCCACAGGTTGCGGCAAATTCCCACAGGTTTCCGCAAATTCTTCTGGGCAACTGGAAGAAATTCCCACAGGTTGCGGCAACTGGCGCAACTGGCCCTAACAATAACTTCTTCTGGGCACACCGCACTTTGGTCGCCAACTACCTAC	1741   GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800   1741   GCTCAATCTGGCCTGTTGGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800   1801   CCGTTTACCTGGCTGACGTTACAAGCGCTAACCGCAAGCTGTAT 1800   1801   CCGTTTACCTGGGATGCCGTAACGTTACAAGCTGATTGCTTACCCGATCGCTGTT 1860   1811	1921   GAGNTCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGACCGCTGATGTTCAAC
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Zinc finger protein; ZFP; gene expression; metabolic pathway regulator; modulation; plant technology; agriculture; ds.
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note= "CDS does not include start and stop codon"
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bound moiety= "F1-f1 primer"
824. 72889
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bound_moiety= "F3-bl primer"
953. 3021
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992. 3042
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076. 3141
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205. .3273
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867. _2940
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bound_moiety= "F5-b primer"
119. _3192
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                               AAD11589 standard; DNA; 3300 BP
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168. .3225
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (EPP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target nucleotide sequence, where the expression of the target gene in the plant cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with partial sequence of pMal-m2 and ZFPm2 DNA New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of Example 4; Page 140-142; 156pp; English P-PSDB; AAE06002 

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	Db 3241 ACCGGTAAAAAACTAGTGGCCAGGCCAGTACCGTACGACGTTCCGGACTACGCT 3300 RESULT 6 AAH25681 standard; DNA; 8101 BP. XX AC AAH25681; XX DT 05-SEP-2001 (first entry) XX DT 05-SEP-2001 (first of human Cdc25C phosphatase DNA.
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               maltose binding protein; MBP; Cdc25C phosphatase;
t; Cdc25B3; cyclin-dependent kinase; CDK; cell division;
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 9-13; 56pp; French
                                                                                                                                                                                                14-DEC-1999; 99FR-00015722.
30-MAY-2000; 2000FR-00006883.
21-SEP-2000; 2000FR-00012008.
                                                                                                                                                                     13-DEC-2000; 2000WO-FR003496
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                 Fusion protein; me
Cdc25B1; Cdc25B2;
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                                                                              sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents pMAL-HsCdc25C, a plasmid encoding human cdc25C phosphatase. The specification describes the use of aryl-substituted secondary or tertiary amines for the production of medicaments for inhibiting Cdc25 phosphatases, especially Cdc25C phosphatases. The amines of the invention are used for treating spontaneous alopecia or alopecia induced by exogenous products or radiation. They are also used for treating tumoural or non-tumoural proliferative diseases, parasitic diseases, viral infections, proliferative diseases are e.g. anglogenesis, psoriais or restenosis. proliferative diseases are e.g. anglogenesis, psoriais or restenosis. The amines are also useful for inhibiting the proliferation of microorganisms (especially yeasts) and in the treatment of all disorders conventionally treated with vitamin K or its derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cdc25 Phosphatase inhibiting medicaments, useful e.g. for treating diseases, viral infections, neurodegenerative disease or alopecia, containing new or known aryl-substituted amines.
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/note= "encodes maltose binding protein (MBP)"
2713. 4134
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/note= "ORF of human Cdc25C"
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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The invention relates to a purified P30 antigen (1) chosen from 3 fully defined Toxo30de13C, Toxo30de12C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acid sequence in amino acid sequence of Toxo30de13C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-Toxo30de14C(52-294aa) and MBP-Toxo30mIX1 [Toxo30de13C(52-300aa), MBP-Toxo30de14C(52-294aa) and MBP-Toxo30mIX1 [Toxo30de14C(52-294aa) and mBp-Toxo30mIX1] [Toxo30de13C(52-300aa), mBP-Toxo30de14C(52-294aa) and mBp-Toxo30mIX1 [Toxo30de14C(52-294aa)] and mBp-Toxo30mIX1 [Toxo30de14C(52-294aa)] and mBp-Toxo30mIX1 [Toxo40de15C] [Toxo40de15C] [Toxo40de15C] [Toxo40de15C] [Toxo40de15C] [Toxo50de15C]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                          Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIXI, useful for detecting presence of IgM or antibodies to Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 7259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7259 BP; 1870 A; 1822 C; 1926 G; 1641 T; 0 U; 0 Other;
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Bliese TR;
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81.5%; Score 2690.4;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches
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MAINE G T. PATEL C B. GINSBURG S R BLIESE T R.

(PATE/) (GINS/) (BLIE/) (MAIN/)

Page 17

661 301 361 361 421 481 541 601 721 421 481 541 601 661 721 1021 1081 841 196 1081 1141 1201 1201 1261 1261 8 원 ò 요 ò g à g dd 8 8 8 ò qq à 8 à 셤 ò g ò 엄 à g ò 셤 à ద ò 셤 à 셤 ò g The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIX1 sequences, having 1-6 anino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acid sequence in which at least one of Toxo30del3C P30 antigen sequence is substituted amino acid sequence of Toxo30del3C P30 antigen sequence chosen from MBP-Toxo30del3C P30 antigen sequence chosen from MBP-Toxo30del3C P30 antibodise to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of Contanting the IgM antibodies of with a composition comprising (I) and detecting the presence of [I]/IgM antibody complexes. The present sequence represents DNA encoding a MBP-ToxO30 fusion protein of the invention. ö GTCAATTCAGGGTGGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGGTATGCCG 120 9 9 Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30de13C, Toxo30de12C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii. P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1; MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1; Toxoplasma gondii; ds; gene. CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA CGGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 81.5%; Score 2690.4; DB 12; Length 7322; 99.8%; Pred. No. 0; arive 0; Mismatches 6; Indels 0; Sequence 7322 BP; 1887 A; 1844 C; 1934 G; 1657 T; 0 U; 0 Other; .; 0 DNA encoding MBP-ToxoP30dell0(52-284aa) fusion protein. Bliese TR; Ginsburg SR, Example 2; Fig 25; 114pp; English 02-OCT-2002, 2002US-00263153 02-OCT-2002, 2002US-00263153 (first entry) Conservative (MAIN/) MAINE G T. (PATE/) PATEL C B. (GINS/) GINSBURG S R. (BLIE/) BLIESE T R. Maine GT, Patel CB, WPI; 2004-304563/28. P-PSDB; ADO23614. Query Match Best Local Similarity Matches 2694; Conserv Toxoplasma gondii US2004067239-A1 08-APR-2004. Synthetic 61 61 121 181

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1020 480 1320 480 360 420 420 540 900 600 099 99 720 720 780 780 840 840 900 900 960 AACAACTGGCGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC TGGTGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCAAATC TGGTGGTGTCGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGCGGTGCAAATC TTCTCGCGCAACGCGTCAGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCCA TTCTCGCGCAACGCGTCAGTGGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA TIGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTTCTTGATGTCTCTGACCAGA CGCGTCTGCGTTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG CACCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGGGGGTGGAGCATC TGGTCGCATTGGGTCACCAGCAAATCGCGCGTTAAGCGGGCCCCATTAAGTTCTGTCTCGG CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG redrogeatreserchechantesescretrasessescretraserreres TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATAC CGGAACGGGAAGGCGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA 781 ATGAGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA 841 IGCGCCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG 901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 901 ACGATACCGAGAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 961 GCCTGCTGGGGGAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGAAGCCAATGCTTCTGGCG TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCTGGCGCCCCAATA CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel purified polypeptide having sequence identity to amino acid sequence of F910 antigen of Toxoplasma gondii e.g. Toxo30de13C, Toxo30de12C, Toxo230de12C, Toxo230de12C, antibodies to Toxoplasma gondii.
                                                                                                                                                2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
                                                                                                                                                                                                        2581 GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG
                                                                                                                                                                                                                                                                       TTGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAAGGCCCCAGAAAGGTGAAATCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                   CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCTGCTGCGGTGATCAACGCC
                                                                                                                                                                                      GCCAGCGGTCGTCAGACTGTCGATGAAGCCCCTGAAAGACGCGCAGACTAATTCGAGCTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding MBP-ToxoP30del4C(52-294aa) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bliese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ginsburg SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Fig 19; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                        ADO23603 standard; DNA; 7352
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                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MAIN/) MAINE G T.
(PATE/) PATEL C B.
(GINS/) GINSBURG S R
(BLIE/) BLIESE T R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GT, Patel CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-304563/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toxoplasma gondii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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with a composition comprising (I) and detecting the presence antibody complexes. The present sequence represents DNA encod ToxoP30 fusion protein of the invention.  Sequence 7352 BP; 1896 A; 1852 C; 1943 G; 1661 I; 0 U; 0 Othe Nuery Match	Best Local Similarity 99.8%; Stole 2990.%; DB 12; Length 7352; Matches 2694; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGGCATGATAGCGCCCGGAAGAGA 60 	61	121 GTGTCTTATCAGACCGTTTCCCGCGTGAACCAGGCCAGCCA	181 CGCGGGAAAAGTGGCGGCGAAGCGGGAGCTGAATTACATTCCCAACCGCGTGGCACCGCGTGGCACCGCGTGGCACCGCGTGGCACCGCGTGGCACCGCGTGGCACCGCGTGGCAACCGCGCGTGGCAACCGCGCGGAACCGAACGCGGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGAACGCGGAACGCGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGGAACGCGAACGCGAACGCGAACGCAACGCGAACGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGCGAACGAACGCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGAACGCAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCGAACGCCAACACCCAACACCAC	241 AACAACTGGGGGGAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC		361 IGGIGGIGGAIGGIAGAACGAAGCGGCGICGAAGCCIGIAAAGCGGCGGIGCAAATC 420 	421 TTCTCGCGAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 480 	481 TIGCTGTGGAAGCTGCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA 540	541 CACCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGACCATC 600 		661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720 			841 TGCGCGCATTACCGAGTCCGGGCTGCGCGTGCGGATATCTCGGTAGTGGGATACG 900 	901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAACAGGATTTTC 960 
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TGCTGGGGCAAACCAGCGTGGACGCTTGCTGCAACTCTCTCAGGGCCAGGGGGTAA GGAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAAAACCACCCTGGCGCCCAATA .CAATTCTCATGTTTGACAGCTTATCATCGACGGTGCACGATGCTTCTGGCG AAACCGCCTCTCCCCGCGCTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT  us-09-765-555b-18.rng

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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acid sequence in which at least one of Toxo30del3C P30 antigen sequence chosen from MBP-Toxo30del3C(52-200aa), MBP-Toxo30del3C(52-294aa) and MBP-Toxo30del3C(52-300aa), MBP-Toxo30del4C(52-294aa) and MBP-Toxo30MIX1 fusion proteins. (I) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-ToxoP30 fusion protein of the invention.
                                                                                                                     Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACCCATCAACAGTATTATTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGGATC
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Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7370 BP; 1901 A; 1855 C; 1949 G; 1665 T; 0 U; 0 Other;
                                   Bliese TR;
                                     Ginsburg SR,
                                                                                                                                                                                                                 Example 2; Fig 15; 114pp; English
                                                                                                                                                                               antibodies to Toxoplasma gondii.
                                   Patel CB,
                                                                   WPI; 2004-304563/28
P-PSDB; ADO23599.
BLIESE T R.
                                     Maine GT,
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                                                                                                                                                                                                                                                                                       AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT
                                                                                                                                                                                                                                                                                                                                                             P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding MBP-ToxoP30del3C(52-300aa) fusion protein.
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TCAGGCACCATCGGAAGCTGTGGTGTGTGTGTGTGTGTGT		2341
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                                                                                 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG
                                                                                                                        TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA
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                                                 P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, Toxo830 MIXI, useful for detecting presence of IgM or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7370 BP; 1900 A; 1856 C; 1950 G; 1664 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
                         DNA encoding MBP-ToxoP30MIX1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 2690.4;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                              Bliese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                              SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Fig 31; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                          antibodies to Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                              Ginsburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81.5%;
99.8%;
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                                                                                                                                                                                                                                02-OCT-2002; 2002US-00263153
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Matches 2694; Conservative
                                                                                                                                                                                                                                                          MAINE G T.
PATEL C B.
GINSBURG S R.
BLIESE T R.
                                                                                                                                                                                                                                                                                                                              Maine GT, Patel CB,
                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-304563/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                       gondii
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01-JUL-2004
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The invention relates to a purified P30 antigen (1) chosen from 3 fully defined Toxo30de13C, Toxo30de12C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30de13C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-Toxo30de13C(52-300aa), MBP-Toxo30de14C(52-294aa) and MBP-TOXO30MIX1 fusion proteins. (1) is useful for detecting the presence of Igm
                                              GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
                        GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG
                                                                                                   CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
                                                                                                                                                              CGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
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                                                                                                                                                                                                                  AACAACAACAACAATAACAATAACAACCTCGGGATCGAGGGAAGGATTTCAGAATTC
                                                                                                                                                                                                                                                                           Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, Toxo930 MIX1, useful for detecting presence of IgM or IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bliese TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding MBP-ToxoP30MIX5 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
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P-PSDB; AD023650.
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                                                                                                      ATTGTGAGCGGATAACAATTTCACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA
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plasma gondii in a test sample, which involves t sample suspected of containing the IgM antibodies comprising (I) and detecting the presence of (I)/IgM . The present sequence represents DNA encoding a MBP-tein of the invention.  1900 A; 1857 C; 1950 G; 1663 T; 0 U; 0 Other;  81.5%; Score 2690.4; DB 12; Length 7370;  99.8%; Preed No. 0;  varive 0; Mismatches 6; Indels 0; Gaps 0;	TCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGGA 60	120 180 240	300 300 360 360		TRGACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA 540  [	TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCG 660  TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGCCCATTAAGTTCTGTCTCG 660  TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGCCCATTAAGTTCTGTCTCGG 660  CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720  CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720  CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720	780 780 840 900 900
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                                                          TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding MBP-ToxoP30MIX3 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AD023644 standard; DNA; 7370
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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30de13C, Toxo30de12C and Toxop30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acid sequence in amino acid sequence of Toxo30de13C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-Toxo30de13C(52-300aa), MBP-Toxo30de14C(52-294aa) and MBP-Toxo30mIX1 fusion proteins. (I) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-Toxo930 fusion protein of the invention.
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                                                                                                                                                                                                                   Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
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Matches 2694; Conservative
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AD023594 standard; DNA; 7403

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                                                                                                                                                                                      P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300ae); MBP-Toxo30del4C(52-294ae); MBP-Toxo30MIX1;
Toxoplasma gondii; de; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 6; Indels 0;
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                                                                                                                                                 DNA encoding MBP-ToxoP30del2(52-311aa) fusion protein.
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(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
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                                             AACAACTGGCGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTGC
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Db 2341 CCGAACAAGAGCTGGCAAAACTATCTGCTGACTGATGATGAGGTTG 2400  Qy 2401 GAAGCGGTTAATAAAGACAAACGGTGGCTGACTGACTGATGAGGAAGG 2460  Db 2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCTGAAGTCTTACGAGGAAGG 2460  Qy 2461 TTGGCGAAGATCCACGTATTGCCGCTGCGTGAGCTTATACGAGGAAGAG 2460  Qy 2461 TTGGCGAAGATCCACGTATTGCCGCCACTAGGAAAACGTCAAGTCTTACGAGGAAGAG 2520  Qy 2521 CCGAACATCCCGCAGATGCCGCTTTCTGGTATGCCGTGCTACTGCGGTGAAATCATG 2520  Qy 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCTACTGCGGTGATCAACGCC 2580  Qy 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCTACTGCGGTGATCAACGCC 2580  Qy 2581 GCCAGCGGTCGTCAGACTTCTGGTATGCCGTGCTACTGCGGTGATCAACGCC 2640  Qy 2581 GCCAGCGGTCGTCAGACTGTCCGATGAAGACGCCAGAACTAATTCCAACGCC 2640  Qy 2641 AACAACAACAACAATAACAACAACAACACCCTGAAAGACGCCAGACTAATTCCAGATTC 2700  Db 2641 AACAACAACAACAATAACAACAACACCTCGGGATCGAGGATTTCAGAATTC 2700  Db 2641 AACAACAACAACAATAACAACAACACCTCGGGATCGGGGATTTCAGAATTC 2700  Db 2641 AACAACAACAATAACAATAACAACACCTCGGGATCGAGGGATTTCAGAATTC 2700	Search completed: August 1, 2005, 04:28:59 Job time : 1101.6 secs							
1261   TCAGGCAGCCATCGGAAGCTGTGCAGGTCGTAAATCACTGCATAATTCG   1320	621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGAAAACTGGAAGAAATTCCCACAGGTT	41	1801 CGTTTACCTGGGTGCCTAACGTTACAACGCAACGCTGATTGCTTACCCGATCGCTGTT 1860 1861 GAAGCGTTATCGCTGATTATAAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 1861 GAAGCGTTATCGCTGATTTATAAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGCAAACCCGCCCAAAAACCTGGGAA 1920	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980		2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAACACACATGAATGCAGACACGATTAC 2160	1 TCCATCGCAGAAGCTGCCTTTAATAAGGCGAAACGGGATGACCATCAACGGCCCGTGG  1 TCCATCGCAGAAGCTGCTTTAATAAAGGCGAAACGGGTGTGAACGGTACATCAACGGCCCGTGG  21 GCATGGTCCAACATCGACAACAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC	2281 AAGGTCAACCATCCAAACCGTTCGTTGGCGTGAGCGCAGGTATTAACGCCGCCAGT 2340
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MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: El PR PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,036
FILING APPLICATION 1530
PRIOR APPLICATION NUMBER: GB 9623908.2
FILING APPLICATION NUMBER: GB 9623908.2
FILING ATE: 18-NOV-1996
ATTOMNEY/AGENT INFORMATION:
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US-08-125-462-2
US-08-181-468-2
US-08-181-848-5
US-09-128-314-4
US-09-102-86-56-208
US-09-072-56-208
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Attwood, Michael R
APPLICANT: Hurst, David N
APPLICANT: Hurst, David N
APPLICANT: Jones, Philip S
APPLICANT: Kay, Paul B
APPLICANT: Raynham, Tony M
APPLICANT: Wilson, Francis X
TITLE OF INVENTION: Amino Acid Derivatives
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 38522
REGISTRATION NUMBER: 38522
REERERNEC/DOCKET NUMBER: RAN 4430/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 235-4387
TELEPRAX: (973) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
                                                                                                                                                                                                                                                                                                                                                                          US-08-971-036-1; Sequence 1, Application US/08971036; Patent No. 586684; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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GTRANDEDNESS: double
   CITY: Nu.
STATE: N.J.
COUNTRY: U.S.A.
TP: 07110
   US-08-971-036-1
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Sequence 2, Appli
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Sequence 784, App
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'Gqn2 6/ptodata1/ina/5B_COMB.seq:*
'Gqn2 6/ptodata1/ina/6A_COMB.seq:*
'Gqn2 6/ptodata1/ina/6B_COMB.seq:*
'Gqn2 6/ptodata1/ina/RB_COMB.seq:*
'Gqn2 6/ptodata1/ina/PCTUS COMB.seq:*
'Gqn2 6/ptodata1/ina/PCTUS COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-06-570-1

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US-09-640-882-2

US-09-640-882-3

US-08-148-675A-2

US-08-148-675A-2

US-08-148-675A-2

US-08-148-675A-2

US-08-103-35

US-08-103-35

US-09-702-705-785

US-09-736-457-785

US-09-736-457-785

US-09-736-457-785

US-09-671-124B-785

US-09-671-124B-785

US-09-671-124B-785

US-09-68-184-785

US-09-671-325-784

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US-09-68-184-784
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Maximum Match 100%
Listing first 45 summaries
                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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	661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720 661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720 661 CGCGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCTGGATAG 720 721 CGGAACGGGAAGGCGACTGGACTGCCATGCTAAATTCAAATTCAAATTCAGCTGAAATGCTGA 780 722 CGGAACGGGAAGGCGACTGGACTGCCATGTCCCGATTTTCAAAATGCTGAATGCTGA 780 781 ATGAGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCAA 840 781 ATGAGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCAA 840 781 TGCGCGCCATTACCGAGTCCGGATGCTGGTTGCTGAACGATCAGATGGCGCAA 840 841 TGCGCGCCATTACCGAGTCCGGGCTGGCGGTTGGTGCGAATCAGATGGCGGCAA 840 841 TGCGCGCCATTACCGAGTCCGGGCTGGCGGTTGGTGCGGATACTCGGTAGTGGGGAATTTC 960 841 TGCGCGCCATTACCGAGTCCGGGCTGGTTGGTGCGGATACTCGGTAGTGGGGATTTC 960 841 TGCGCGCCATTACCGAGTCCGGGCTGGTTGGTGCGGATACTCGGTAGTGGGGATTTTC 960 841 TGCGCGCCATTACCGAGTCGGGCTGGTTGATGCGGATACTCGGTAGTGGGGATTTTC 960 841 TGCGCGCCATTACCGAGTCGGGCTGGTGGTGGGGATATCTCGGTAGTGGGGGTAA 1020 842 TGCGCGCCATTACCGAGTCGGGGTGGACCGCTTGATGCGGCATACAACCAGGTTGTTTATATCCCGGCGGTTAACCACCACTCAAACAGGGGGTGA 1020 843 TGCGCGCCATTACCGGGCTGGTGGACCGCTTGCTGCACCCTCTCTCAGGGCGGTGA 1020 844 TGCGCGCCATTACCGGGGGAGCCGCTTGCTGCAGCCCTCTCTCAGGGCCAGGCGGTGA 1020 851 GCCTGGTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACCACTCTCTCAGGGCCAGGCGGTGA 1020 865 GCCTGTTGGGGCAAACCAGCGTGGACCGCTTGCTGCAAACTCTCTCT

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Patent No. 6372883
GENERAL INFORMATION:
APPLICANT: Attwood, Michael R.
APPLICANT: Gnes, Philip S.
APPLICANT: Kay, Paul B.
APPLICANT: Kay, Paul B.
APPLICANT: Kay, Paul B.
APPLICANT: Raynam, Tony M.
APPLICANT: Raynam, Tony M.
APPLICANT: Raynam, Tony M.
APPLICANT: Raynam, Tony M.
CURRENT PRING NO. Antiviral Medicaments
FILE REFERENCE: 20052 antiviral medicaments
FILE REFERENCE: 20052 antiviral medicaments
CURRENT APPLICATION NUMBER: US/09/265,617B
CURRENT PILING DATE: 1999-03-10
PRIOR FILING DATE: 1998-03-03
NUMBER OF SEQ ID NOS: 24
SORTWARE: Patentin Ver. 2.0 RESULT 3 US-09-265-617B-1 1921 1921 1981 2041 2101 2101 2161 2161 2221 2281 2341 2521 2581 1981 2041 2221 2281 2341 2401 2401 2461 2461 2521 유 8 6 8 6 8 8 8 8 6 8 P 6 ઠે g à g ð g δ g 1020 1080 1140 1200 1260 1500 1020 1260 1320 1320 1380 1380 1560 1560 1620 1620 1680 1680 1740 1800 1800 1860 1860 960 960 GAAGGGITAICGCIGAITTATAACAACAICTGCIGCCGAACCCGCCAAAAACCIGGGAA 1920 900 TGCGCGCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGGATACG ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTGGTAAATCACTGCATAATTGG TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT GCACTTCACCAACAAGAGCCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAAATCTGG 

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NAME: Brown, Anne
REGIGYRATION NUMBER: 36,463
REFERENCE/DOCKET NUMBER: 5789-3
TELECOMMUNICATION INFORMATION:
TELEPAX: 919 813175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5926 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
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Matches 1455; Conserv
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                                                                                             2101 GGTCTGACCTTCCTGGTTGACTTAAAAACAAACAACACATGAATGCAGACACGGTTAC
                                                                                                                                         2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
                                                                                                                                                                                                                                                                              CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACGATGAAGGTCTG
                                       TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
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                         TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGGAAAGCG
                                                                           GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09027169
Fatent No. 6420524
GENERAL INFORMATION:
TITLE OF INVENTION: GAIN OF FUNCTION MUTATIONS IN
TITLE OF INVENTION: ATP-DEFENDENT TRANSPOSITION PROTEINS
TUTLE OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE Anne Brown (Alston & Bird, LLP)
STREET: 3605 Glenwood Ave.
CITY: Raleigh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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// MOLECULE TYPE: other nucleic acid
// DESCRIPTION: /desc = "pEM delta R.adj to 1"
US-09-027-169-3
                                                                                                                 13.0%; Score 1417.6; llarity 98.6%; Pred. No. 0; Conservative 0; Mismatches
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| Patent No. 5720142
| GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Hall, Barry G. 1711LE OF INVENTION: MESTSTANCE GENES AND USE THEREOF TO SCREEN FOR DRUG TITLE OF INVENTION: EFFICACY: FILE REFERENCE: 176/60851
| FILE REFERENCE: 176/60851
| CURRENT APPLICATION NUMBER: 06/149,813
| PRIOR PILING DATE: 2000-08-18
| PRIOR APPLICATION NUMBER: 60/149,813
| PRIOR FILING DATE: 1999-08-19
| NUMBER OF SEQ ID NOS: 17
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 2
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                                                          GATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGC
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TYPE: DNA
CREAMISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: pACSE2
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243 CAACTGGGGGGAAACAGTGGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCAC 302 1106 CAACTGGGGGGAAACAGTCTGTTGCTGATTGGCTATGTCACTCTAGAACAGTCTAGAAAAAGTGATGAAAAAAAA	GCGCCGTCGCAAATTGTCGCGCGGTTAAATCTCGCGCCGATCAACTGGCGTG	1166 GCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCGTG 1225 363 GTGGTGTCGATGGTAGAACGAACGAGCGCGTCGAAGCCTGTAAAGCGGGGGGGG	1226 GIGGIGICGATGGTAGAACGAGCGGCGCTCGAAAGCGGCGGCGGCGCACAATCTT 1285 423 CTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGAATGCCATT 482	CTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCGCTGGATGACCAGGATGCCATT	483 GCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA 542	543 CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGACTGGGCGTCGGAGCATCTG 602 1406 CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCAACTGGACGTACAGCGAACTAGAACGAAC				783 GAGGGCATCGTTCCCACTGCGATGCTGGCTAACGATCAGATGGCGCTGGGCGCAATG 842 	843 GGGGCATTACCGAGTCCGGGCGTTGGTGCGGATATCTCGGTAGTGGGGATACGAC 902	903 GATACCGAAGACAGGTCATGTTATATCCGGCGGTTAACCACTCAAACAGGATTTTGGC 962 	963 CTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGGGGTGAAG 1022	1023 GGCAATCAGCTGTTGCCGTCTCACTGGTGAAAAAAAAAA	1083 CAAACCGCCTCTCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTTCC 1142	1143 CGACTGGAAAGCGGGCAGTGACGCAATTAATGTGAGTTAGCTCACTCA	1203 ACAAITCICAIGITIGACAGCITAICAIGGACTGCACGGTGCACCAAIGCTICTGGCGTC 1262 	1263 AGGCAGCCATCGGAAGCTGTGGTATGGCTGTGGGAGGTCGTAAATCACTGCATAATTCGTG 1322	
<i>&amp;</i> 8	ò	a y	qa X	qu (	ð 8	ò 8	ර් දි	& 8 €	දු පු	ob ob	P 6	oy Db	Oy Op	ò a	S q	δ O	\$ A	& d	ò
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ATTILE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
ATTILE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                        2243
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STRAIN: BL21 (DE3)
FUBLICATION INFORMATION:
AUTHORS: NOBUYUKI FUJII ET AL,
TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: PROM SID FUSED DNA SEQUENCE AND METHOD OF
TITLE: REPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 4557
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UNDBER: US/08/778,717
FILING DATE: 12-DEC-1996
CLASSIFICATION: 536
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APPLICATION NUMBER: JP 352225/1995
FILING DATE: 28-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2084-031-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHMAN: 703-413-3000
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                                                                                                                                                                           S-08-778-717-5
Sequence 5, Application US/08778717
Patent No. 6602689
GENERAL INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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US-08-487-283A-18/c
; Sequence 18, Application US/08487283A
; Patent No. 6355245
; GENERAL INPORMATION:
; APPLICANT: Evans, Mark J.
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                                                                                                                                                                                              Sequence 2, Application US/08148675A

Patent No. 5505121

GENERAL INFORMATION:
APPLICANT: Skerra, Arne; Schmidt, Thomas
ITILE OF INVENTION: STREPTIDES WITH BINDING ACTIVITY FOR TITLE OF INVENTION: STREPTAVIDIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
COUNTRY: USA
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36.4%; Score 1200.8;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1202; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 BOCMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDSEFECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/148,675A
FILING DATE: 3-NOV-1993
CLASSIFICATION A435
PRICA APPLICATION DATA:
APPLICATION NUMBER: DE 42 37 113.9
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
FILING DATE: 03-NOV-1992
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 688-9200
TELEFAX: (212) 688-9200
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                                                              GCAC 1204
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US-08-148-675A-2
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US-08-148-675A-2
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                       ACGCCCCCTCCCAAATTGTCGCGCCGATTAAATCTCGCCCCGATCAACTGGGTGCCAGCG
                                                                                   4450 TGGTGGTGTCGATGGTAGAACGAAGCGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATC
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 PCT-US96-05611A-21/C
; Sequence 21, Application PC/TUS9605611A
; GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Lenardo. Michael J.
APPLICANT: Meraland, Henry P.
APPLICANT: Matis, Louis A.
APPLICANT: Matis, Louis A.
APPLICANT: Mueller, Eileen Elliott
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 ACGCGCCGTCGCAAATTGTCGCGCCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360
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APPLICANT: Matis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Nother, Russell P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Thomas, Thomas C.
APPLICANT: Thomas, Thomas C.
APPLICANT: Thomas, Thomas C.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: OF INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.3%; Score 1199.2; DB 3; Length 5248; 99.8%; Pred. No. 0; ative 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Circular
MOLECULE TYPE: Other nucleic acid
DESCRIPTION: DET Trc SO5/NI
DESCRIPTION: prokaryotic expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUTURNIA APPLICATION DATA:
APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
FILING DATE: June 7, 1995
FILING DATE: June 7, 1995
ATPOINTENANTHER: US 08/236,208
FILING DATE: 02-MAY-1994
ATPOINTEX/AGENT INFORMATION:
NAME: Seth A. Fidel.
REGISTRATION NUMBER: 38,449
FELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 1776-1790
TELEFRAX: (203)772-3655
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.4Mb storage
COMPUTER: Macintosh Cetris 610
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
                                                                                                                                                                                                                                                  E: Seth A. Fidel
25 Science Park (Alexion)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEC 1D NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 5248 base pairs TYPE: Nucleic Acid STRANDEDNESS: Double
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                                                                                                                                                                                                                                                                                                             Connecticut
: USA
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STREET: 25 Scien
CITY: New Haven
                                                                                                                                                                                                                                                                                                                                                 ZIP: 06511
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US-08-487-283A-18
                                                                                                                                                                                                                                                                                                                           COUNTRY:
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4510 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 4451
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Patent No. 6817723
GENERAL INFORMATION:
APPLICANT: AVENTIS PASTEUR
APPLICANT: Chevalier, Michel
APPLICANT: RI Habib, Raphaelle
APPLICANT: Krell, Tino
APPLICANT: Krell, Tino
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US-10-263-103-35/c
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APPLICANT: Mys, oleven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
APPLICANT: Wilkins, James A.
APPLICANT: Wilkins, James A.
APPLICANT: Wilkins, James A.
ANDRER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CTTY: Pairfield
STATE: Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prokaryotic expression vector
                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: System 7

OPERATING SYSTEM: System 7

CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/482,114
                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Circular MOLECULE TYPE: Other nucleic acid DESCRIPTION: per Trc SOS/NI DESCRIPTION: prokaryotic express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: KIEE, MAULICE M.
REGISTRATION NUMBER: 30,39
REFRENCE/DOCKET NUMBER: ALX-
TELEPHONE: (203) 255 1400
INFORMATION: (203) 255 1101
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: Double
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Best Local
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                                                                                                ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfratin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,967
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99.8%; Pred. No. 0;
iive 0; Mismatches
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CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REPRENCE/DOCKET UNBER: P103!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 5443 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity 99.8
Matches 1201; Conservative
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36.3%; Score 1199.2;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1201; Conservative 0; Mismatches
TITLE OF INVENTION: gp41 antigen
FILE REFERENCE: 01-1692-A
CURRENT APPLICATION NUMBER: US/10/263,103
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 5312
                                                                                                                                                 TYPE: DNA
ORGANISM: Artificial
PEATURE:
OTHER INFORMATION: plasmid pET-cer
US-10-263-103-35
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                                                                                                                                                                                                Score 1199.2;
Pred. No. 0;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SEQ TWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 785
LENGTH: 5502
                                                                                                                                                                                                   Query Match
Best Local Similarity 99.8%;
Matches 1201; Conservative C
                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-785
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                                                              4197 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGGGTTATTTCTTGATGTCTCTGACCAGA
                                                                                                                                          CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC
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Sequence 785, Application US/09736457

GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

APPLICANT: Lodes, Michael A.

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick

APPLICANT: Retter, Marc

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APPLICANT: Retter, Marc

APPLICANT: Mannion, Jane

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                                                     TGGTGGTGTCGATGGTAGAACGAAGGGGTCGAAGCCCTGTAAAGCGGCGGTGCACAATC
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                                                                       AGGGAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAACCACCCTGGCGCCCAATA
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      ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
                                                     GCCTGCTGGGGGAAACCAGCGTGGACGGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
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| Patent No. 6630574
| GENERAL INPORMATION:
| APPLICANT: Wang, Tongtong
| APPLICANT: Bargur, Chattanya S.
| APPLICANT: Chattanya S.
| APPLICANT: Carter, March Tonger, Tom
| APPLICANT: Carter, March Tonger, Tom
| APPLICANT: Carter, March Tonger, Tom
| APPLICANT: Mannion, Jane
| APPLICANT: Mannion, Jane
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
| TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
| TITLE OF INVENTION: 12.47829|
| TITLE OF INVENTION: 12.47829|
| TITLE OF INVENTION: 12.47829|
| TITLE OF INVENTION: 16.09|
| FILE REFERENCE: 210.1.47829|
| TURRENT FILING DATE: 2001-07-11
| NUMBER OF SEQ ID NOS: 16.69
| SOFTWARE: FREESEQ for Windows Version 3.0
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Pred. No. 0;
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Best Local Similarity 99.8%;
Matches 1201; Conservative (
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US-09-614-124B-785
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Total number Minimum DB E Maximum DB E

Database

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Sequence 40, Appl
Sequence 31, Appl
Sequence 25, Appl
Sequence 20, Appl
Sequence 61, Appl
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Sequence 17, Appl
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US-09-765-555-18
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TITLE OF INVENTION: Methods and compositions to modulate;
TITLE OF INVENTION: Expression in plants
FILE REPERENCE: 27801-20014.40
CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT FILING DATE: 2002-05-24
FRIOR APPLICATION NUMBER: US 09/620,897
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,468
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 3300
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iive 0; Mismatches
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Publication No. US20030037355A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Score

Result

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US-09-765-555-17
                   RESULT 2
US-09-765-555-17
US-09-765-555-17
Sequence 17, Application US/09765555
; Publication No. US2003003735A1
; GENERAL INFORMATION:
APPLICANT: The Scripps Research Institute
; TITLE OF INVENTION: Methods and compositions to modulate
; TITLE OF INVENTION: Methods and compositions to modulate
; TITLE OF INVENTION: METHOD NOWBER: US/09/765,555
CURRENT PILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 69/620,897
; PRIOR PILING DATE: 2000-01-21
; PRIOR PILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FASESEQ for Windows Version 4.0
; SEQ ID NO 17
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US-09-765-555-14
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Publication No. US20030037355A1

GENERAL INFORMATION:
TITLE OF INVENTION: Methods and compositions to TITLE OF INVENTION: expression in plants
FILE REFERENCE: 27801-20014.40

CURRENT APPLICATION UNMERS: US/09/765,555

CURRENT FILING DATE: 2002-05-24

PRIOR APPLICATION NUMBER: US 09/620,897

PRIOR APPLICATION NUMBER: US 60/177,468

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 75

SOFTWARE: FARISEG for Windows Version 4.0

SEQ ID NO 14
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tive 0; Mismatches
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	1441 ATTGTGAGGGATAACAATTTCACACAGGAAACAGCCAGTCTAGGTGTTTTCACGA 1500 1441 ATTGTGAGGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 1441 ATTGTGAGCGGATAACAATTTCACACAGGAACAGCCGGTCGGT		CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTACCCCGATCGCTGT  [	CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCGCGCGTTATGCGTTCAGG 204  CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGAGGGGTTATGCGTTCAGG 204  CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGAGGGGGTTATGCGTTCAGG 204  TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 210  TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCTGGATAACGCTGGCGCGAAAGCG 210  GGTCTGAACCTTCCTGGTTGACGTTAAAAAACAAACACTGGATAACGCTGCGCGAAAGCG 210  GGTCTGACCTTCCTGGTTGACCTGATTAAAAAACAAACAA	2161 TCCATCGCAGAAGCTGCCTTTAATAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220  2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGTGG 2220  2221 GCATGGTCCAACATCGACAACAGCAAATATGGTGTAACGGTACTGCCGTGG 2220  2221 GCATGGTCCAACATCGACAACAGCAAATTATGGTGTAACGGTACTGCCGACCTTC 2280  2221 GCATGGTCCAACATCGACAACAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280  2281 AAGGGTCAACCATCGATGGTTGGTTGGTGTGAGCGCAGGTATTAACGCCGCCAGT 2340  2281 AAGGGTCAACCATCCAAACCGTTGGTTGGTGTGAGCGCCAGGTATTAACGCCGCCAGT 2340  2281 AAGGGTCAACCATCCAAACCGTTGGTTGGTGTTGAGCGCAGGTATTAACGCCGCCAGT 2340
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                                                                                                                                                                                                             Length 3300;
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                                                                                                                                                                   zinc finger
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                                                                                                                                                                                                             DB 10;
                                                                                                                                                                  and
                                                                                                                                                                 OTHER INFORMATION: Partial sequence of pMal-m2 OTHER INFORMATION: protein ZFPm2
                                                                                                                                                                                                          Query Match 97.8%; Score 3226.4;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 3254; Conservative 0; Mismatches
TITLE OF INVENTION: expression in plants
FILE REFERENCE: 27801-20014 40
CURRENT APPLICATION NUMBER: US/09/765,555;
CURRENT FILING DATE: 2002-05-24
FRIOR FILING DATE: 2000-01-21
FRIOR FILING DATE: 2000-01-21
FRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PSESEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 3300
                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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1861   GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA   1920   1861   GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCCAAAAACCTGGGAA   1920   1921   GAAGCGTTATCGCTGATTTTATAACAAAGATCTGCTGCTGCCGCCCCAAAACCTGGGAA   1920   1921   GAGATCCCGGCGCTGATTGTTCAAC   1980   1921   GAGATCCCGGCGCTGATTGATCTGAAAGAAACGAAAAGAAAG	GCATGGTCCAACATCGACACCAGCAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC  [	2611 AACAACAACAATAACAATAACAACAACCTGGGGAAGGAATTTGAGAATTC 2700 2611 AACAACAACAACAATAACAATAACAATAACAACAACAGGGAAGGGAATTTGAGAATTC 2700 2611 AACAACAACAACAATAACAATAACAACACCTGGGGAAGGGATTTGAGAATTC 2700 2701 GGATCCTCTTCCTCTGTGGCCCAGGGGGCCTCGAGCCCGGGGAAGCCCTATGCTTGT 2760 2701 GGATCCTCTTCCTCTGTGGCCCAGGGGCCCTCGAGCCCGGGGAAGCCCTATGCTTGT 2760 2761 CCGGAATGTGGTAAGTCCTTCAGCCAGGGGCCCTGGGGGAGAAGCCCTATGCTTGT 2760 2761 CCGGAATGTGGTAAGTCCTTCTCAGAGGCCCTCGGGGGAGAAGCCCACAGGGTACCCAC 2820 2761 CCGGAATGTGGTAAATGCCCAGAGGGCCCTCGGTGGCCCACAGGGTACCCAC 2820 2821 ACGGGTGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTAGCCAGCAGCCAGC

1381 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440 	1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 	1501 GCACTTCACCAACGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG 1560 	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAGAT 1620 	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 	1681 GCGCCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACCGCTTTGGTGGCTGC 1740	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTTT 1800 	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGT 1860 	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980 	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040 	2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGGGATAACGCTGGCGCGAAAGCG 2100 	GGTCTGACCTTCCTGGTTGACCTGATTAAAACAAACATGAATGCAGGACACCGATTAC 	TCCATGGCAGAAGCTGCCTTTAATAAAGGCGAAACAGGATGACCATCAACGGCCCGTGG 	2221 GCATGGTCCAACATCAGCAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280	H-H	CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA	2401 GAAGGGGTTAATAAAGACGGCTGGGTGCGTGAGGTCTTACGAGGAAGAG 2450 
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PEATURE:
OTHER INFORMATION: Expression vector pMalc2cchbmp2
                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
             Patentin Ver. 2.1
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Publication No. US20040087524A1
APPLICANT: Wiederanders, Bernd
APPLICANT: Wiederanders, Gunter
TITLE OF INVENTION: Agent for postoperative use after removal of bone tumors
FILE REPERBNCE: 2045-101
CURRENT APPLICATION NUMBER: US/10/257,384A
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: PCT/DE 01/01510
PRIOR PILING DATE: 2001-04-18
PRIOR PILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 19
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  TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG
                         2461 TIGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG
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PERTURE:

NAME/KEY: CDS

LOCATION: (1528)...(3453)

OTHER INFORMATION: /product = fusion protein MBP Cystatin C BMP-2
FEATURE:

NAME/KEY: misc feature
LOCATION: (2689)
OTHER INFORMATION: Faktor Xa Protease /position=388
OTHER INFORMATION: (Amino acid sequence)
FEATURE:
NAME/KEY: misc feature
LOCATION: (3067)...(3108)
OTHER INFORMATION: (Spacer between Cystatin C andBMP-2
FEATURE:
NAME/KEY: misc feature
COTHER INFORMATION: (Spacer between Cystatin C andBMP-2
FEATURE:
NAME/KEY: misc feature
COTHER INFORMATION: (Spacer between Cystatin C andBMP-2
FEATURE:
NAME/KEY: misc feature
COTHER INFORMATION: (Spacer between Cystatin C andBMP-2
FEATURE:
NAME/KEY: M B.
TITLE: Expression vector pMal-X, complete sequence
JOURNAL: Anal: Biochem.
VOLUME: 264
ISSUES: 1998-11-01
PAGES: 87-97
DATE: 1998-11-01
PAGES: 87-97
DATE: 1998-11-01
FEEVANT RELEVANT RESIDUES: 1528 - 3453
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                                                                                      Sequence 5, Application US/10149472

Publication No. US20040029204A1

GENERAL INFORMATION:

APPLICANT: GOUBLN-CRAMATICA, FRANCOISE

APPLICANT: DUCOMMIN, BERNARD

APPLICANT: DUCOMMIN, BERNARD

APPLICANT: PREVOST, GREGOIRE

TITLE OF INVENTION: MCHENORE BENTIFYING HUMAN CDC25 PHOSPHATASE AND METHOD

TITLE OF INVENTION: FOR IDENTIFYING HUMAN CDC25 PHOSPHATASE AND METHOD

TITLE OF INVENTION: FOR IDENTIFYING HUMAN CDC25 PHOSPHATASE MODULATORS

TITLE OF INVENTION: FOR IDENTIFYING HUMAN CDC25 PHOSPHATASE MODULATORS

CURRENT APPLICATION NUMBER: US/10/149,472

CURRENT PILING DATE: 2000-12-13

PRIOR PELING DATE: 2000-12-14

PRIOR APPLICATION NUMBER: FR 99/15722

PRIOR APPLICATION NUMBER: FR 00/06883

PRIOR APPLICATION NUMBER: FR 00/06883

PRIOR APPLICATION NUMBER: FR 00/12008

PRIOR APPLICATION NUMBER: FR 00/12008

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Qy 2701 GGATCCTCT 2709            Db 2701 GGATCCTCT 2709	RESULT 8 US-10-343-859-8 ; Sequence 8, Application US/10343859 ; Publication No. US20040110161A1 ; GENERAL INFORMATION: ; APPLICANT: Nanogen Recognomics GMBH ; TITLE OF INVENTION: Method for detecting mutations in		PRIOR FILING DATE: 2001-07-13  PRIOR FILING DATE: 2000-08-04  PRIOR FILING DATE: 2000-08-04	NUMBER OF SEQ ID NOS SOFTWARE: PatentIN V SEQ ID NO 8 LENGTH: 6648	Artificia DRMATION:	pMAL-CZX 81.8%;	Cocal Similarity 99.8%; Pred. No. 0; ss 2704; Conservative 0; Mismatches 5; Indels	Oy 1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60	Qy         61 GTCAATTCAGGGTGGTGAAACGTGAAACCAGTAATACGATGTCGCAGAGTATGCCG         120           Db         61 GTCAATTCAGGGTGGTGAATGTCAAACCATAATACGATGTCGCAGAGTATGCCG         120	121 GIGTCTCTTATCAGACCGTTTCCCGCGTGGACCAGGCCAGCCA	Db 121 GTGTCTCTTATCAGACCGTTTCCCGCGTGGTGACCAGGCCAGGTTTCTGCGAAAA 180 Qy 181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240		QY         241 AACAACTGGCGGCAAACAGTCGTTGCTGATTGGCGTTGCCACTCCAGTCTGGCCCTGC         300           Db         241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACTCCAGTCTGGCCTGC         300	Qy 301 ACGCGCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGGCCGATCAACTGGGTGCCAGCG 360	Db 301 AGGGCGTCGCAAATTGTCGCGGGATTAAATCTCGCGCGGATCAACTGGGTGCCAGGG 360  Qy 361 TGGTGGTGGTAGAAGGAAGGGGGGGGGGGGGGGGGGGG	Db 361 TGGTGGTGTCGATGGTAGAACGAAGCGGCGGTCGAAAGCCTGTAAAGCGGCGGTGCACAATC 420	421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA	DB 421 TICTCGCGCAACGCGTCAGTGGGCTTGATCGTTCGCTGGATGACCAGGATGCCA 480 Qy 481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGGGTTATTTCTTGATGTCTCTGACCAGA 540	Db 481 TTGCTGTGGAAGCTGCCAGAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA 540	Qy 541 CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC 600
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GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGATAT CGGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATCATCAAC CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGGTGACGGGGGTTATGCGTTCAAG CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT GAGATCCCGGCGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAAACCCGGCCAAAAACCTGGGAA GGTCTGACCTTCCTGGTTGACCTGATTAAAACAAAGACACATGAATGCAGACACCGATTAC GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAAACGGTACTGCCGACCTTC 2341 CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGATGAAGGTCTG GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG GCATGGTCCAACATCGACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG TIGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAACGCCCAGAAAGGTGAAATCATG CGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2581 GCCAGCGGTCGTCAACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC GGATCCTCT 2709 GGATCCTCT 

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US-10-343-859-9
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99.8%; Pred. No. 0;
iive 0; Mismatches
                       US-10-343-859-9

Sequence 9, Application US/10343859

Sequence 9, Application US/10343859

Publication No. US20040110161A1

GENERAL INFORMATION:
APPLICANT: Nanogen Recognomics GMBH

TITLE OF INVENTION: Method for detecting mutt;
TITLE OF INVENTION: Muclectide sequences
FILE REFERENCE: 612,406-033

CURRENT APPLICATION NUMBER: US/10/343,859

CURRENT FILING DATE: 2001-07-13

FRIOR APPLICATION NUMBER: 10038237.1

PRIOR APPLICATION NUMBER: 10038237.1

PRIOR APPLICATION NUMBER: 10038237.1

PRIOR FILING DATE: 2000-04

NUMBER OF SEQ ID NOS: 52

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 9

LENGTH: 9191
                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
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Matches 2701; Conservative
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TYPE: DNA
ORGANISM: Toxoplasma gondii
FEATURE:
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                                  CCGTTTACCTGGGATGCCGTACGTTACAACGCCAAGCTGATTGCTTACCCGATCGCTGTT
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                                                    CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT
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GENERAL INFORMATION:

APPLICANT: Abbort Laboratories

APPLICANT: Abbort Laboratories

APPLICANT: Patel, Chandu B.

APPLICANT: Patel, Chandu B.

APPLICANT: Patel, Chandu B.

APPLICANT: Patel, Chandu B.

TITLE OF INVENTION: GINBURGY, SANIFORN R.

ITLE OF INVENTION: GENERALICALLY ENGINEERED P30 ANTIGEN,

ITLE OF INVENTION: GENERALICALLY ENGINEERED P30 ANTIGEN,

ITLE OF INVENTION: GENERALICALLY ENGINEERED P30 ANTIGEN,

ITLE OF INVENTION: GENERALICALLY ENGINEERED P30 ANTIGEN,

INTLE OF INVENTION UNMERS: US/10/263,153

CURRENT FILING DATE: 2002-10-22

NUMBER OF SEQ ID NOS: 74

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 40

LENGTH: 112 DB 18; Length 7112; ö 6; Indels ; LOCATION: (1528)...(3189) ; OTHER INFORMATION: pMBP-c2X-ToxoP30dell1 (52-214aa) US-10-263-153-40 Query Match
81.5%; Score 2690.4;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 601 661 요 8

1711 GCTCAATCTGGCCTGTAACCCGCAAAACCCGCAAAACCTGTTATT 1860     1801 CCGTTTAACCTGGATGCCGTAACCCGCAAAACCTGTTT 1860     1801 CCGTTTAACCTGGATTACCAACGCCAACCTGATTACTTAC	RESULT 11 US-10-263-153-30 i Sequence 30, Application US/10263153 j Publication No. US20040067239A1 j GENERAL INFORMATION: i APPLICANT: Abbott Labbratories j APPLICANT: Maine, Gregory T. j APPLICANT: Patel, Chandu B. j APPLICANT: Ginsburg, Sanford R. j APPLICANT: Bliese, Timothy R.
COGNICTOGGENERACY TRANSCRIPTION	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT 1680 1681 GCGGCAACTGGCCATGGCCTGACATTATCTTCTGGGCACACGACTTTGGTGGCTAC 1740 1681 GCGGCAACTGGCGTGGCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTAC 1740 1681 GCGCAACTGGCGTGGCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTAC 1740 1741 GCTCAATCTGGCTTGGCTGACATTATCTTCTGGGCACACGCTTTGGTGGCTAC 1740 1741 GCTCAATCTGGCTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800

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            ATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA
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TITLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REFERENCE: 6984.03.01
CURRENT APPLICATION WUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
SUFFRENT FILING DATE: 2002-10-22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH... 7259
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; OTHER INFORMATION: pMBP-c2X-ToxoP30de14de18 (83-294aa)
US-10-263-153-30
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81.5%; Score 2690.4;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches
                                                                                                                     TYPE: DNA
ORGANISM: Toxoplasma gondii
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NAME/KEY: CDS
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                                                                       NAME/KEY: CDS

1. LOCATION: (1528)...(3399)

2. OTHER INFORMATION: pMBP-c2X-ToxoP30dell0 (52-284aa)

MS-10-263-153-35
                                                                                                                                              Score 2690.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                              Query Match
Best Local Similarity 99.8%;
Matches 2694; Conservative
SEQ ID NO 35
LENGTH: 7322
TYPE: DNA
ORGANISM: Toxoplasma gondii
FEATURE:
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US-10-263-153-35
is Sequence 35. Application US/10263153
is Sequence 35. Application US/10263153
is Publication No. US20040067239A1
is GENERAL INFORMATION:
is APPLICANT: Maine, Gregory T.
is APPLICANT: Patel, Chandu B.
is APPLICANT: Bilese, Timochy R.
is APPLICANT: Ginsburg, Sanford R.
is APPLICANT: Ginsburg, Sanford R.
is TITLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
if TILE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
is FILE REFERENCE: 6994.US.01
is CURRENT PILING DATE: 2002-10-22
is NUMBER OF SEQ ID NOS: 74
is SOFTWARE: FastSEQ for Windows Version 4.0
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901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAACAGGATTTTC 960 901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAACAGGATTTTC 960 901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACACACA	

CCGACACCATCGAAAGCCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60	181 CGCGGGAAAAAGTGGAAGCGGGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 24	241	301 ACGCGCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGGCCGATCAACTGGGTGCCAGCG 360 	361 IGGIGGIGTGTCGAIGGIAGAACGAAGCGCGTCGAAGCTGIAAAGCGGCGGGGGCAATC 420 	421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAAGATGCA 480	481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA 540	541 CACCCATCAACAGTATTATTTTCCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC 600 	601 TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTG	661 CGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720 	721 CGGAACGGGAAGGCGACTGGAGGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA 780 	781 ATGAGGGATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAA 840 	841 TGCGCGCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG 900 	901 ACGATACCGAAGACGCCTCATGTTATATCCCGCCGTTAACCACCATCAACAGGATTTTC 960 	961 GCCTGGTGGGGAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGTGA 1020 	1021 AGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAAACCACCCTGGCGCCCAATA 1080
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Qy         2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACAATGAATG	234	AGGTCTG			9y 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580				sequence zo, Application US/10263153 ; Publication No. US20040067239A1 ; GENERAL INFORMATION: ; APPLICANT: Abbott Laboratories	APPLICANT: Patel, Chegory T. ; APPLICANT: Patel, Chandu B. ; APPLICANT: Ginsburg, Sanford R. ; APPLICANT: Bliese, Timothy R.	111LE OF INVENTION: GENETICALLY ENGINERED P30 ANTIGEN, 1 TILE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF 1 FILE REFERENCE: 6984.US.01 1 CURRENT APPLICATION NUMBER: US/10/263,153	CURRAIN FILING DATE: 2002-10-22  NUMBER OF SEQ ID NOS: 74  SOFTWARE: FASESEQ for Windows Version 4.0  SEQ ID NO 20	JENGHI, 7370  TYPE: DNA ORGANISM: Toxoplasma gondii	MACHAN ARX   (1528) (3447)	Query Match 81.5%; Score 2690.4; DB 18; Length 7370; Best Local Similarity 99.8%; Pred. No. 0; Matches 2694; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db   2161 TCCATCGCAGAAGCTGTTTAATAAAGGCGAAACGGGTGTGAACGGCCCGTGG 2220   Qy   2221 GCATGGTCCAACATCGACACGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280	2281 AAGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT	Qy 2341 CCGAACAAAGGCTGGCAAAAGGGTTTCCTCGAAAACTATCTGCTGATGATGATGATGTGTTG 2400	2401 GAAGGGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG 	2461 TIGGCGAAAGAICCACGTATIGCCGCCACCAIGGAAAACGCCCAGAAAGGIGAAAICATG [	2521 CGGAACHTCCGGAGATGTTCGGGTTTCTGGTGTGCGTGCGTGCGTGGTGATCAACGCC	2581 GCCAGCGGTCGTCAACTGTCAATGAAGCCCTGAAAGACGGCAGACTAATTCGAGCTCG [	Oy 2641 AACAACAATAACAACAACAACACCCGGGATGGGGAGGATTTCAGAATTC 2700	RESULT 15 US-10-263-153-61 ; Sequence 61, Application US/10263153	; Publication No. US20040067239A1 ; GENERAL INFORMATION: ; APPLICANT: Abbott Laboratories ; APPLICANT: Maine, Gregory T.		; TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF; FILE REPERENCE: 6984 US.01. ; CURRENT APPLICATION NUMBER: US/10/263,153 ; CURRENT FILING DATE: 2002-10-22	; NUMBER OF SEQ ID NOS: 74 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 61 ; LENGTH: 7370	; TYPE: DNA ; PGGANISM: Toxoplasma gondii ; FEATURE: ; NAME/KEY: CDS	(3447) pMBP-c2X-ToxoP30MIX1	Query Match 81.5%; Score 2690.4; DB 18; Length 7370; Best Local Similarity 99.8%; Pred. No. 0; Matches 2694; Conservative 0; Mismatches 6; Indels 0; Gaps 0;	Qy 1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAG 60	Qy         61 GTCAATTCAGGGTGGTGAAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120
		1201 GCACAATTUTCATGTTTGACAGCTTATCATCGACTGCACGGTGCCACTGCTTCTGGCG 1260 1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320 1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320	TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTGCGCCGACATCATAACGGTT 	1381 CTGGCAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440 	1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 	1501 GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG 1560 	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGT 1620 	1621 ACCGGAATTAAAGTCACCGTTGAGCATCGGGATAAACTGGAAGAAATTCCCACAGGTT 1680 	1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGGCTTTGGTGGCTAC 1740 	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800 	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGGATCGCTGTT 1860 	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980 	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCTGGGGGGGTTATGCGTTCAAG 2040 	2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGC 2100 2041 TATGAAAACGCGAACTTACCACATTAAAAACATAAAAAAAA	GGTCTGACCTTCCTGGTTGACCTGATTAAAACAAACATGATGAGGGGCCCGGTTAC	CCCGTGG
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	1 CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA	1 ccgaacaaagagcrgccaaaagagrrccrcgaaaacrarcrgcrgacrga	1 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG 2460	GAAGGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG 2460	1 TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520	1 TTGGCGAAAGATCCACGTATTGCCGCCACTATGGAAAACGCCCAGAAAGGTGAAATCCATG 2520	1 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580	1 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCTACTGCGGTGATCAACGCC 2580	1 GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640	GCCAGCGGTCGTCAGATGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640	1 AACAACAACAACAATAACAATAACAACCTCGGGATCGAGGGAAGGATTTCAGAATTC 2700	1 AACAACAACAACAATAACAATAACAACCTCGGGATCGAGGGAAGGGATTCAGAATTC 2700	
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Colletotrichum trifolii
SM Colletotrichum trifolii
EMARYOFAS Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.

EE (Dassel Lo 794)
Samac,D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T., Cheung,F. and Fraser,C.M.
ESTS from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
Other ESTS: ST5612498
Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesoca
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA Feat: 651 659 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAH67TV More information is available at:
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Seq primer: (gtA AtA CgA CtC ACt AtA ggg C).
Location/Qualifiers
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Listing first 45 summaries
                                                    OM nucleic - nucleic search, using sw model
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BJ063872
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CL655575
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9b est2:

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Match Length
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E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."
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                                                                                                                                              GACACTTTCGAATGGCGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGT
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23.6%; Score 778; DB 5; L
Best Local Similarity 98.7%; Pred. No. 3.4e-219;
Matches 784; Conservative 0; Mismatches 10;
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CK394523 779 bp mRNA linear EST 30-DEC-2003 hggada4D08 Gland Cell Amplified cDNA Library Heterodera glycines

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Heterodera glycines
Bukaryota, Metazoa, Nematoda, Chromadorea, Tylenchida, Tylenchina,
Tylenchoidea, Heteroderidae, Heteroderinae, Heterodera.
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/db_xref="taxon:51029"
/cell_type="gland"
/cell_type="gland"
/clone lib="gland cell Amplified cDNA Library"
/note="Organ: gland cell; Vector: pSportII"
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Pred. No. 5.3e-217;
0; Mismatches 5;
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1. .779
/organism="Heterodera
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Heterodera glycines Gland
                                  CK394523
CK394523.1 GI:40389794
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Best Local Similarity 99.4%;
Matches 773; Conservative (
mRNA sequence
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EST632218 DSCT Colletotrichum trifolii cDNA clone pDSCT6-59, mRNA
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Colletotrichum trifolii
Colletotrichum trifolii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
1 (bases 1 to 793)
Samac, D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,
Cheung,F. and Fraser,C.M.
ESTS from mycella of Colletotrichum trifolii race 1
Unpublished (2002)
                                                                                                                     541 ATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCGGGGGTGG
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JOURNAL
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BQ751220
EST631783 DSCT Colletotrichum trifolii cDNA clone pDSCT3-64, mRNA
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                 GCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA 542
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/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK+; Site_1: EcoRI; Site_2:
EcoRI; isolate: 28p2; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtll from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
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S Samac.D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,
Cheung,F. and Fraser,C.M.

ESTS from mycelia of Colletotrichum trifolii race 1
Unpublished (2002)
OCHET_ESTS: ESTS: 31782
Conteact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, U
Tel: 612 625 1243
Fax: 651 649 5088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colletotrichum trifolii
Colletotrichum trifolii
Colletotrichum trifolii
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Colletotrichum.
                                                                                               CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTG
                                                                                                                                541 CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGGGACTGGGCGTGGAGGATCTG
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TIGR sequence name: MTSAC64TV More information is available
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/organism="Colletotrichum trifolii"
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Seg primer: (gtA AtA CgA CtC ACt AtA ggg
Location/Qualifiers
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BQ751220.1 GI:21906625
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/clone_libs_Boscr.
/clone_libs_Boscr.
/notes_Weetor: pBluescript SK+; Site_I: EcoRI; Site_2:
EcoRI; isolate: 28p2 ; cDNA was prepared from polyA+
enriched RNA The cDNA was ligated into Lambda gtil from
Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y109 and phage DNA was purified from a liquid
lyaate. The CDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
                                                                                           MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mycelia"
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               Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN.
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAF59TV More information is availab
www.medicago.org
Seq primer: (gtA AtA CgA CtC AtA ggg C).
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                                                                                                                                                                                                                                                                   /organism="Colletotrichum trifolii"
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clone="pDSCT6-59"
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  Other_ESTs: EST632217
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Best Local Similarity 99.11
Matches 777; Conservative
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RESULT 6
CB863541/c
LOCUS CB863541 689 bp mRNA linear EST 22-APR-2003
DEFINITION HH04A08y HH Hordeum vulgare cDNA clone HH04A08 3-PRIME, mRNA
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lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."
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                                                                              Length 806;
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                                                                              Score 755.4; DB 5;
Pred. No. 1.8e-212;
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Hordeum vulgare
Hordeum vulgare
Hordeum vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae,
Pooideae, Triticeae, Hordeum.
1 (bases 1 to 689)
Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTCTTATCAGACCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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/dev_stage="coleoptile, 1 day old"
/lab_host="DH108"
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/mol type="mRNA"
/cultivar="Sloop"
/db_xref="GAB1:555198"
/db_xref="GAB1:555198"
/clone="HH04A08"
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: stein@ipk-gatersleben.de
Insert Length: 689 Std Error:
Plate: 4 row: A column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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AY080106
AY080106 Scripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3G6L, genomic survey
                                                                                                                                                                          TGGCGTTGCCACTCCAGTCTGGCCCTGCAC-GCGCCGTCGCAAATTGTCGCGGCGATTA 330
                                                                                                                                GCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTGAT 473
          652 ACGTTATACGATGTCGCAGAGTATGCCGGTGTCTTTATCAGACCGTTTTCCCGCGTGGTG 593
                                                                                                           GCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTGAT 271
                                                                                                                                                                                                  TCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATCA 450
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1 (base i to 710)

Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Mead, D., Azam, F. and Rohwer, F. Genomic analysis of uncultured marine viral communities Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
                                                                 AACCAGGCCAGCCACGTTTCTGCGAAAACGCGGG-AAAAAGTGGAAAGCGGCGATGGCGGA
                                                                                                                                                                                                                                          331 AATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTCGATGGTAGAACGAAGCGGCG
                                                                                                                                                                                                                                                                                                                                         rcgaagccrgraaagcggcggrgcacaarcrrcrcgcgcaacggcacagrgcarca
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Biology Dept.
San Diego State University
S500 Campanile Dr. San Diego, CA 92102, US.
Tel: 6195941336
Fax: 619595576
Fmail: forcet@sunstroke.sdeu.edu
Class: shotgun.
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DKPZp566E0346_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566E0346_5', mRNA sequence.
                    560
                                                                                     209 ACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGAGACACCCATCAACATATTT 150
                                                                                                                                         620
                                                                                                                                                                                                CAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCGTCTGGCC 680
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1 (bases 1 to 712)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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TTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAG
                                                                                                                                                   89 CANATCGCGCTGTTAGCGCGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCGTCTGGCTCGGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        available.
This clone (DKFZp566E0346) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                501 ACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 GGTATGGCATGATAGCGCCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAAACCAGTA
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20.5%; Score 676.4; DB 1;
Best Local Similarity 99.6%; Pred. No. 5.3e-189;
Matches 699; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                  TGGCATAAATATCTCACTCGCAATCAAAT 709
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Contact: MIPS
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19.6%; Score 647.4; DB 1;
99.7%; Pred. No. 2.2e-180;
iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp4341102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="testis"
                                                                                                                                                                                    EST (Ansorge, Benes, et al.)
Unpublished (1999)
                                            AL044483.1 GI:5432701
                                                                              Homo sapiens (human)
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659; Conservative
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                                                                         /note="Marine viruses were isolated from 200 liters of surface seawater using a combination of differential filtration and density-dependent gradient centrifugation. Linker-amplified shotgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating dsDNA linkers to the ends, and amplifying the fragments using Vent DNA polymerase. The resulting fragments were ligated into the pSMART vector and electroporated into MC12 cells (Lucigen; Middleton,
                                                                                                                                                                                                                                                                                                                                                       67
/mol_type="genomic DNA"
/db_xref="taxon:186617"
/clone="SIO513G6L"
/clone="SIO513G6L"
/clone_lib="Scripps Pier (La Jolla, CA) uncultured virus
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                                                                                                                                                                                                                                                               Score 676; DB 8; Length 71
Pred. No. 6.9e-189;
0; Mismatches 7; Indels
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98.9%;
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Best Local Similarity 98.9
Matches 690; Conservative
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144 601 204 541 264 481 324 421 384 361 444 504 241 360 GCGGCGTCGAAGCCTGTAAAGCGGCGGCGTGCACAATCTTCTCGCGCAACGGGTCAGTGGGC 301 Euteleostomi; Ansorge, W., Benes, V., Krieger, S., Mewes, H.W., Gassenhuber, J. and Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 3' sequence of the clone insert Clone From S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email 8 wiemann@dkfz- heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. No rI sequence available.
This clone (DKFZp4341102) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de. 145 GCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAAACGCGGGAAAAAGTGGAAGCGGCGA 600 GCGIGGTGAACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTGGAAAGCGGCGA 265 TGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCGCCGTCGCAAATTGTCGCGG ceartraaarcrcececearcaacreeereccaecerecreererearceareeragaaceaa 85 AACCAGTAACGTTATACGATGTCGCAGAGTATGCCGGTGTCTTTATCAGACCGTTTCCC TGGCGGGAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGT 480 TGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCCTGCACGCGCCCGTCGCAAATTGTCGCGG CGATTAAATCTCGCGCCGATCAACTGGGTGCCCAGCGTGGTGGTGGTAGGAACGAA Gaps /dev stage="adult" /lab\_host="DH10B" /clone\_lib="434 (synonym: htes3)" /note="Vector: pSport1; Site\_1: Not1; Site\_2: Sal1" DKFZp434I102\_s1 434 (synonym: htes3) Homo sapiens cDNA clone DKFZp434I102\_3', mRNA sequence. Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo ï Length 660; Indels 셤

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505 ATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTTTTCT

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EST 04-SEP-2003

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CB863814 62-2003
HH07B20y HH Hordeum vulgare cDNA clone HH07B20 3-PRIME, mRNA
                                                              210 GAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTG 269
                                                                                                                                        329
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Hordeum vulgare
Hordeum vulgare
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.

1 (bases 1 to 624)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 GAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTG
                                                                                                                                 270 ATTGGCGTTGCCACCTCCAGTCTGGCCCTGCACGCCCGTCGCAAATTGTCGCGGCGATT
                                                                                                                                                    330 AAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGGTAGAACGAAGCGGC
                                                                                                                                                                                                                                  341 AAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGGTGGTAGTAGAACGAAGCGGC
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                                                                                                                                                                                                                                                                                                                                      161 CCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCAT
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Unpublished (2003)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Correnser. 3, 06466, Gatersleben, Germany
Tel: 039482-5525
Eax: 039482-5525
Email: stein@ipk-gatersleben.de
Insert Length: 624 Std Error: 0.00
Plate 7, row: B column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 CTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTGCG 670
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/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Sloop"
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|db_xref="taxon:4513"
|clone="HH07B20"
|/tissue_type="coleoptile"
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The information of this clone is available through the following
                                                 CCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACAGCAAA
                                                                                                                     625 regegererrangegegecentrangurergreregegegegererggerggergege
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="whole embryo"
/dev stagg="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadaeu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

19.4%; Score 641; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 1.7e-178;
Matches 641; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .641
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL077k02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://xenopus.nibb.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 81-559-81-6855
Email: tshini@genes
                                                                                                                                                                                                                                                        745 C 745
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BJ063872/c
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); sequenced by Qiagen within the cDNA
sequencing consortium of the German Genome Project. rl sequence
also available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
1. 794
/organism="Homo sapiens"
/db xref="taxon.9606"
/clone="DKFZp4348075"
//dor.n="type="testis"
//dor.n="type="testis"
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                                                                                                                                                                                                                                                                                                                                                                         /dev stage="adult"
/lab_host="bH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sal1"
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99.7%; Pred. No. 7.6e-170;
iive 0; Mismatches 0;
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   EST (Duesterhoeft,
Unpublished (1999)
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Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
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                                 /clone lib="HH"
/note="Vector: pSPORT; Site 1: SalI (5-end of cDNA);
/note="Vector: pSPORT; Site 1: Due to the cloning system site." NotI (3-end of cDNAT, Due to the cloning system used blue/white selection for recombinants is not 100 % reliable. Average insert size is 1.3 kb."
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DKFZp434B075_3', mRNA sequence.
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                                                                                                                                                                 Score 615.8; DB 6; Length 624;
Pred. No. 5.3e-171;
0; Mismatches 2; Indels 0
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/dev_stage="coleoptile,
/lab_host="DH108"
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PRIO124a CO1 - PRIO124a.B21 (752) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic
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                                                                                                                                                            Eukaryota; Metazoa; Mematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.

1 (bases 1 to 752)

Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J. AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus

L Nucleic Acids Res. 32 (1), D421-D422 (2004)

Conteact: Sommer RJ

Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 3-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fex: 00497071601378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                       Sommer, R.J.
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                                                                                                                                                                                                                                                                                                                                                                         Email: raif sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and
sequenced at Vancouver, Canada.
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18.3%; Score 603; DB 9; Length 752;
Best Local Similarity 98.9%; Pred. No. 3.6e-167;
Matches 628; Conservative 0; Mismatches 5; Indels
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Organism="Prietionchus pacificus"
/mol_type="genomic DNA"
/strain="california"
                                                                                                                                                                                                                                                                                                                                                                                                                      Seq priner: T7
Seq priner: T7
Class: fosmid ends.
Location/Qualifiers
                                                                                                  CL655575.1 GI:50134897
                                                                                                                             Pristionchus pacificus
Pristionchus pacificus
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                              1. .608
/organism="uncultured marine virus"
/mol_type="genomic DNA"
/db_xref="taxon:186617"
/clone="S1051p33b4L"
/clone="S1051p33b4L"
/clone_lib="Scripps Pier (La Jolla, CA) uncultured virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           surface seawater using a combination of differential tiltration and density-dependent gradient centrifugation. Linker-amplified shorgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating dsDNA linkers to the ends, and amplifying the fragments using vent DNA polymerase. The resulting fragments were ligated into the pSMART vector and electroporated into MC12 cells (Lucigen; Middleton,
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Mead, D., Azam, F. and Rohwer, F.
Proc. analysis of uncultured marine viral communities
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY080094
AY080094 Scripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3D4L, genomic survey
                                                                                                    CACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATGCCGAACATCCCGC
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                                                                                                                                                                                                                                                                                                                  2594 AGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT 2628
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Biology Dept.
San Diego State University
5500 Campanile Dr. San Diego, CA 92102,
Tel: 6195941336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 619595676
Email: forest@sunstroke.sdsu.edu
Class: shotgun.
Location/Qualifiers
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uncultured marine virus
Viruses; environmental samples.
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completed: August 3, 2005, 02:02:54
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DKFZp564C157_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DKFZp564C157_5', mRNA sequence.
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1 (bases 1 to 589)
Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF3); Email 8 wiemann@dkf2- heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd
Braunschweig/Germany) within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No 81 sequence available.

This clone (DKFZp564C157) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERNANY; Email: clone@rzpd.de. Location/Qualifiers
                                                      AAGTTCTGTCTCGGCGCGTCTGCGTCTGGCTGGCTGGCTAAATATCTCACTCGCAATCA
                                                                                                                                                                                                                                                                                          CATGCAAATGCTGAATGAGGCATCGTTCCCACTGCGATGCTGCTGCCAACGATCAGAT
GGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATT
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                                                                                                                                                                                                                                                                                                                                                                                                      CATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCTGGTTGCCAACGATCAGAT
                                                                                                           TGACCAGGATGCCATTGCTGCAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGA
                                                                                                                                                                 TGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACT
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/mol_type="mRNA"
/db xref="taxon:9606"
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EST (Bloecker, et al.)
Unpublished (1999)
Contact: MIPS
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No 81 sequence avail:
This clone (DKFZp5640
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                                                                                                                           Length 589;
/tissue_type="brain"
/dev stage="fetal"
/lab_host="X1-2blue"
/clone lb="564 (symonym: hfbr2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2:
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                                                                                                                           Score 586.4; DB 1;
Pred. No. 2.8e-162;
0; Mismatches 2;
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AY219682 Shuttle e
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AY493834 Sequence
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Patent: WO 0152620-A 17 26-JUL-2001;
Patent: WO 0152620-A 17 26-JUL-2001;
DISCOVERY, INC. (CA)
Location/Qualifiers
1. 3300
/ organism="synthetic construct"
//mol_type="unassigned DNA"
//db_xref="taxon:33630"
//db_xref="taxon:33630"
//db_xref="Partial sequence of pMal-m4 and zinc finger protein
ZFPM4"
AX768200 Sequence
AX768202 Sequence
AX768203 Sequence
AF140577 Integrati
AX431576 Sequence
AY219686 Expressio
AY219688 Expressio
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CQ846977 Sequence
AX478528 Sequence
AB116367 Expressio
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AX768202
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AY219688
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AX172306 Sequence
AX377531 Sequence
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AF031813 Expressio
CQ794769 Sequence
CQ846980 Sequence
AX768201 Sequence
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17238.272 Million cell updates/sec
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AUTHORS Barbas, C.F., Stege, J.T., Guan, X. and Dalmia, B.  TITLE Methods and compositions to modulate expression in plants JOURNAL Patent: WO 0152620-A 18 26-JUL-2001; The Scripps Research Institute (US); SYNGENTA AGRICULTURAL DISCOVERY, INC. (CA) FEATURES Location/Qualifiers 13300 /organism="synthetic construct" //db zref="taxon:32630" //db zref="taxon:32630" //noce="parial sequence of pMal-Ap3 and zinc finger protein ZFPAp3"	Query Match Query Match Query Match Best Local Similarity 98.0%; Pred. No. 0; Bast Local Similarity 98.7%; Pred. No. 0; Matches 3258; Conservative 0; Mismatches 42; Indels 0; Gaps 0; Qy 1 CCGACACCATCGAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAG 60	61 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAATGGTTATACGATGTGGCGGGGGGGG	181 CGCGGAAAAAGTGGAAGCGGCATGCGGAGCTGAATTACATTCCCAACCGCGTGGCACTTCCGAGGAGCGGGGGGGG	301 ACGCCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCC 301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 361 TGGTGGTCGTAGAAGCGGCGTCGAAGCCGCTGTAAAGCGGCGGTGCAAATC 1611111111111111111111111111111111111	421 TTCTCGCGCAACGCTCATGCTCATAACTATCCGCTGGATGACGGCGGTGCAAATCCA 48 421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 48 481 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 48 481 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCTGGATGACCAGGATGCCA 54	Db 481 Qy 541 Db 541 Qy 601	
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	sc_feature	misc_feature 30673108 /note="/spacer zwischen Cystatin C und BMP-2" ORIGIN	Query Match 82.0%; Score 2705.8; DB 6; Length 7373; Best Local Similarity 99.2%; Pred. No. 0; Matches 2719; Conservative 0; Mismatches 22; Indels 0; Gaps 0;	Qy 1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60	Qy 61 GTCAATTCAGGGTGGATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120	OY 121 GIGICICITATCAGACCGITICCCGCGIGGAGCAGCCAGCCACGITICIGCGAAAA 180	Oy 181 CGCGGGAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACGGGTGGCG 240	Qy         241 AACAACTGGCGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTGC         300           Db         241 AACAACTGGCGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCTTGC         300	QY 301 ACGCGCCGTCGCAATTGTCGCGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360	Oy 361 TGGTGGTGTCGATGGTAGAACGAAGCGGCTGGAAGCCGGCGGGGGGGG	Qy 421 TICTCGGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 480	Qy 481 TIGCTGIGGAAGCTGCCTGCACTAATGITCCGGGGTTAITTCTTGATGTCTCTGACCAGA 540	Qy         541         CACCCATCAACAGTATTATTTTCTCCCATGAACAGTACGCGACTGGGCGTGGAGCATC         600           Db         541         CACCCATCAACAGTATTATTTTCTCCCATGAACAGCGACTGGGCGTGGAGCACTCGACGCACTGGGCGTGCAACCGCACTGGGCGTGCAACCGCACTGGGCGTGCAACCGCAACTGCGCACTGGGCAACCGCAACTAACT	Qy         601         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG         600         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG         600         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG         600         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG         600         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGCCCCATTAAGTTCTGTCTCGG         600         TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGCCCCATTAAGTTCTGTCTCGG         600         TGGTCGCATTGGGTCACAAATCGCGCTGTTAGCGGGCCCATTAAAGTTCTGTCTCGG         600         TGGTCGCATTGGGTCACAAATCGCGCTGTTAGCGGCCCAATTAAGTTCTGTCTCTGG         600         TGGTCGCATTGGGTCACAAATCGCGCTGTTAGCGGGCCCAATTAAAGTTCTGTCTCTGG         600         TGGTCGCATTGGGTCACAAATCGCGCTGTTAGCGGGCCCAATTAAACTTCTGTCTCTCGG         600         TGGTCGCATTGGTCACAAATCGCGCTGTTAGCGGGCCCCAATTAAACTTCTGTCTCTCGG         600         TGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	Qy         661 CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAT	9y 721 CGGAACGGGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA 780	9y 781 ATGAGGGGATGGTTCCCACTGCGATGCTGGTTGCCAAGGATGGCGGTGGGGGAA 840
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              Location/Qualifiers
1. 8101
/organism="synthetic construct"
/mol_type="unassigned DNA"
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/note="souche JM109 / pMAL - Hs C
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 2707; Conservative
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                                  Score 2701; DE
Pred. No. 0;
0; Mismatches
/note="Plasmid pMAL-c2x"
                                  Query Match
Best Local Similarity 99.8%;
Matches 2704; Conservative
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Method for detecting mutations in nucleotide sequences
Patent: WO 021253-A B 14-FEB-2002;
Nanogen Recognomics GmbH (DE)
Location/Qualifiers
1. .6648
| .organism="synthetic construct"
| /mol_type="unassigned DNA"
| /db_xref="taxon:32630"
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                                                   TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
                                                                                   GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACGGTTAC
                                                                                                GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC
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                                  TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
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961 GCCTGCTGGGGCAAACCAGGGTGGACGGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1020 1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAAAAA	CGCAAACGCCTCTCCCCGCGCGTTGCCGCTTAATGCAGCACCGCAGGCTTTAATGCAGCTGCAGCAGGTTTTAATGCAGCTGCAGCAGGTTTTAATGCAGCTGCAGCAGGTTTTAATGCAGCTGCAGCAGGTTTTAATGCAGCTGCAGCAGAAGGTTTTAATGCAGCTGAAGGAAG	ATTAG	16606 16606 16606			1381 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGCTCGTATAATGTGTGTG	1441 ATTGTGAGCGGATAACAATTTCACACAGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 	10166 	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGAT 1620 	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT 1680 		1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTT 1800 	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 	GAGATCCCGGCGCTGGATAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC		1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGGTTATGCGTTCAAG 2040 2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100	2041 TATGAAAACGGGAAGTACGACATTAAAGACGTGGGCGTGGGTATAAACGCTGGCGCGAAAGGC 2100

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1321   TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT   1380	ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCAACGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCAACGGAATTAAAGTCACGGATTAAACTGGAAGAAATTCCCGGGAACTGGGAACTGGGAAGAAATTCCCGGGAACTGGGAACTGGGAACTGGGAACTGGGAACTGGGAACTGGGAACTGAACGGCAAGAACGATTAACTACCCGAACGGAAGATTGCTTACCCGATCGGATTAACTAAC	1921   GAGATCCCGGCGCTGGATAAAGAAACTGAAAGCGAAGGCGCGCTGATGTTCAAC   1980   1921   GAGATCCCGGCGCTGATAAACGGAAAGCGAAAGGGAAGGTAAGAGCGCTGATGTTCAAC   1980   1921   GAGATCCCGGCGCTGGTTAAAAGGCGAAGGTAAGGCGCGCTGATTCACCTGACGGGGGCTTATAAAG   2040   1981   CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG   2040   1981   CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG   2041   TATGAAAACGGCAAGTACGAATTAAAAACGACTGGGCGTGATTACCTGGCGCGAAAGCG   2100   2041   TATGAAAACGGCAAGTACGAATTAAAAACGAGCTGGGGGTTATGCGTGACGTAACGCTGGCGCGAAAGCG   2100   2101   GGTCTGACCTTCCTGGTTGAATTAAAAACGAGCTGGGCGAAACAGCTGGATAACGCTGGCGCAAAGCG   2100   2101   GGTCTGACCTTCCTGGTTGAATTAAAAACGAGCTGGGCGAAACAGCCGATAACGCCGCAAAGCG   2200   2201   GGTCTGACCTTCCTGGTTGAAAAACGAACACACAAGGACTGAACAGCCGAAACAGCCGATGAATGA

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	RESULT 12 AX377532 LOCUS LOCUS DEFINITION Sequence 9 from Patent WO0212553. AX377532 AX377532 AX377532 AX377532 ACCESSION AX377532 VERSION AX377532.1 GI:19573718 KEYWORDS SOURCE synthetic construct	ORGANISM synthetic construct other sequences; artificial sequences.  REFERENCE 1 AUTHORS Kappel,A., Polakowski,T., Pignot,M., Windhab,N., Behrensdorf,H. and Muth,J.  TILLE Method for detecting mutations in nucleotide sequences JOURNAL Patent: WO 0212553-A 9 14-FEB-2002; Nanogen Recognomics GmbH (DE)	Source 19191    Source 19191   Joganism="synthetic construct"   Joganism="synthetic construct	Query Match Best Local Similarity 99.8%; Pred. No. 0; Best Local Similarity 99.8%; Pred. No. 0; Matches 2701; Conservative 0; Mismatches 5; Indels 0; Gaps 0; Qy 1 CCGACACCATCGAAAGCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAG 60 Dh 1 CCGACACCATCGAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60	61 GTCAATTCAGGGTGGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG	QY         121 GTGTCTTATCAGACCGTTGTGAACCAGCCAGCCACCTTCTGCGAAA 180           Db         121 GTGTCTTTATCAGACCGTTTCCCGGGGGAACCAGCCAGCC	241 AACAACTGGGGGAAACACTTGCTGATTGGCGTTGCCACCCCCTGGCTGG	Oy 301 ACCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA	Qy         481 TTGCTGTGGAAGTGCCTGCACTAATGTTCCGGGGTTATTTCTTGATGTCTCTGACCAGA 540           Db         481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGGGTTATTTCTTGATGTCTCTGACCAGA 540           Qy         541 CACCCATCAACAGTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC 600

**ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT** 

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AF097412 6724 bp DNA circular SYN 28-JAN-2002
Expression vector pMBP-parallell, complete sequence.
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Sheffield, P.J., Garrard, S.M. and Derewenda, Z.S.
Direct Submission
Submitsed (05-07-1998) Molecular Physiology and Biological
Physics, University of Virginia, 4215 Jordan Hall, 1300 Jefferson
Park Avenue, Charlottesville, Virginia 22908, USA
                                                                                                                                                                                                                                              Expression vector pMBP-parallell other sequences; vectors.

(bases 1 to 6724)

Sheffield,P., darrard,S. and Derewenda,Z.
Overcoming expression and purification problems of RhoGDI using family of 'parallel' expression vectors
Protein Expr. Purif. 15 (1), 34-39 (1999)
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Patent: WO 0206306-A 194 24-JAN-2002;
PHARMACIA & UPJOHN COMPANY (US)
Location/Qualifiers
1. .6806
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="fusion protein comprising a maltose binding protein with 125 amino"
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                                                                                                                                                   2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
                          GAAGCGITAICGCIGAITTAIAACAAAGAICTIGCIGCCGAACCCGCCAAAAACCIGGGAA
                                           1861 GAAGCGTTATCGCTGATTTATAACAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA
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                                                                                                                                  CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG
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QY         1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGTTATGCCTTCAAG         2040           1981 CTGCAAGAACCGTACTTCACCTGGCCGTGATTGCTGCTGACGGGGTTATGCGTTCAAG         2040           1981 TATGAAAACGGCAATTAAAGACGTGGCGGATAAGCGTTCAAG         2040           2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGCGGGAAACG         2100           QY         2101 GGTCTGACCTTCCTGGTTGACGATTAAAAACGGTGGATAACGGTGGCGGGAAAGCG         2100           QY         2101 GGTCTGACCTTCCTGGTTGACTTAAAAACCAAACAACATGAATGCAGGCGGGAAAGCG         2160           Db         2101 GGTCTGACCTTCTGGTTGACTTAAAAAACAAAAACAAAAAACAAGAATGCAGACCGTTAC         2160           CV         2161 TCCATCGCAGAAACCTGATTAAAAAACAAAAACAAAAAACAACAAAAAACAAAAAAA	2101 CCATGARGETICCTTTAATAAGGGGAAACGGTGACCATCAAGGGCCGTGG 2161 TCCATGGCAGAAGCTGCCTTTAATAAAGGCGAAACGGGTGACCATCAAGGGCCCGTGG 2221 GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC	Db 2341 CCGAACHAGAGTTCTCGAAACTATTTGCTGAAACTTGTGAAGGTTTG C 2400  Qy 2401 GAAGCGGTTAATAAAGACAAACGCTGGGTGCCGTAGCGCTGAAGTTCTTACGAGGAAGA 2460  Db 2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGA 2460  Qy 2461 TTGGCGAAAGATCCACGTATTGCCGCCACATGGAAAAGTCTTACGAGGAAAAG 2520  Db 2461 TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520  Qy 2521 CCGAACATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG 2520  Qy 2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580  Db 2521 CCGAACATCCCGCAGATGTCCGCTTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580  Qy 2521 CCGAACATCCCGCAGATGTCCGCTTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580  Db 2521 CCGAACATCCCGCAGATGTCCGCTTTTCTGGTATGCCGTGCGGTACTGCGGTGATCAACGCC 2580  Qy 2581 GCCAGCGGTCGTCGATGAAGACCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640  Db 2581 GCCAGCGGTCGTCAGAACTGAAGACCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640	RESULT 15 AF031088 LOCUS DEFINITION SHUTTION APUTION AP031088. G12623821 AF031088.1 G1:2623821 KEYWORDS SOURCE ORGANISM AF031088.1 G1:2623821 KEYWORDS SOURCE ORGANISM AF031088.1 G1:2623821 AF031088.1 G1:2623821  KEYWORDS SOURCE ORGANISM AF031088.1 G1:2623821  AUTHOR SHUTTLE vector pMAL-pIII ORGANISM AUTHOR SHUTTLE vector pMAL-pIII  REFERENCE L (bases 1 to 6706) AUTHOR AUTHOR OFFICE AUTHOR AND BADDAS, C. F. III, Noren C.J. and Scott, J.K.  TITLE TITLE PUBMED PUBMED PUBMED PUBMED PUBMED PUBMED SOURCE C (bases 1 to 6706) AUTHORS AU
B41 TGCGGCCATTACCGAGTCCGGGCTTGGTGCGGATATCTCGGTAGGGATACG   900	1081 CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACGGTTT 1140 1081 CGCAAACCGCTCTCCCCGGCGTTGGCCGATTCATTAATGCAGCTGGCACGACGGTTT 1140 1141 CCCGACTGGAAAGCGGCGTTGGCCAATTCATTAATGCAGCTGGCACGACGTTT 1140 1141 CCCGACTGGAAAGCGGCGAGTGAGCGCAATTAATGTCAGTTAGCTCATTAG 1200	TCAGGCACCCATCGGAAGCTGTGCTGTGCAGGTCGTAAATCACTGCATAATTCG TGTCGCTCAAGGCGCACTCCGGTTGTGGTATGCTGTTTTTTTGCGCCGACATCATAAGGTT TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTTGCGCCGACATCATAACGGTT TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTTGCGCCGACATCATAACGGTT CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA ATTGTGAGCGATAACAATTTCACACAGGAAACAGCCGGTTTAGGTGTTTTCACGA ATTGTGAGCGATAACAATTTCACACAGGAAACAGCGGTTTAGGTGTTTTCACGA ATTGTGAGCGATAACAATTTCACACAGGAAACAGCAGTCCGTTTAGGTGTTTTCACCA GCACTTCACCAACAAGGACATAATTATGAAAACTGAAAACTGGTAATCTGG GCACTTCACCAACAAGAACAGAAC	ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAAATTCGAGAAAGATAACGGCGATAAAGGCTATAACGGCTCTCGAGGTCGCGTAAGGAAATTCGAGAAAGATTCGAGGAAAGATTAAACGGCGTATAACGGTCTCGCTGAAGTCGGAAAGAAA

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                                                                                                                                                                                     CGACACCATGGATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
                                                                                                                                                                                                                                                                                GIGICTCTIATCAGACCGTTTCCCGCGTGGTGAACCAGGCCACGTTTCTGCGAAAA
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                                                                                                                                                                                                                                                    GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG
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                                                                                                                                                    CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                481 TIGCTOTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTTCTTGATGTCTCTCACCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG
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                                                                                                               Gaps
                                                                                                               60;
                                                               Length 6706;
                                                                                                            Indels
                                                                                                         5.
                                                               DB 12;
                                                                                                         0; Mismatches
                                                          Score 2631;
Pred. No. 0;
                                                  79.7%;
97.7%;
                                               Query Match
Best Local Similarity 97.7
Matches 2704; Conservative
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                                                                                                                                                                                                                                                                                                    /translation="MKKLLFAIPLVVPPYSHSADMKIEEGKLVIWINGDKGYNGLAEV
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KAKGKSALMPRIQEBYFTWPLIAADGGYAFKYENGKYDIKDVGVDNKGAKAGITFIUD
LIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNGGTUVLFTEKQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="WEIGHPRVALIPPFAAPCLPVFAHPETLVKVKDAEDOLGARVGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEÄVNKÖKPLGAVALKSYEEELÄK
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                    /note="derived from commercially available vector pMal-p2 [New England Biolabs)"
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/protein_id="AAB86559.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="malE-lacZa fusion"
/product="maltose binding protein-lacZ alpha peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1528. 1581
/gene="malE-lacZa fusion"
/note="M13 secretion signal sequence"
                                                                                                                                                                                                                                        'note="transcriptional repressor"
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/standard_name="M13 origin (+ -)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="malE-lacZa fusion"
/note="MBP-lacZa; MBP modified
secretion signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="malE-lacZa fusion"
note="E. coli gene fusion"
528. .2976
xref="taxon:69327"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="Ptac promoter"
528. .2976
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                                                                                                                      gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="GI:2623823
                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
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/transl_table=11
                                                                                                                 'note="E. coli
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                                                                                                                                                                 'gene="laci"
                                                                                             gene="lacI"
                                                                                                                                                                                                              gene="lacI"
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/gene≖"bla"
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Barbas, C.F., Stege, J.T., Guan, X. and Dalmia, B.
Methods and compositions to modulate expression in plants
Patent: WO 01526204 14 26-UUL-2001;
The Scripps Research Institute (US); SYNGENTA AGRICULTURAL
DISCOVERY, INC. (CA)
Location/Qualifiers
Location/Qualifiers
1 . 3300
/ Organism="synthetic construct"
/ Mol type="unassigned DNA"
/ Ab xreft="taxon:33630"
/ note="Partial sequence of pWal-m1 and zinc finger protein
ZPPm1"
                                          AY21968 EXPRESSIO
AY21968 EXPRESSIO
AY21968 EXPRESSIO
AY219689 EXPRESSIO
AY219682 EXPRESSIO
AY219683 Shuttle e
AY219684 Shuttle e
AY219684 Shuttle e
AF177933 Cloning v
AF177932 Cloning v
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AY289542 Expressio
AR49383 Sequence
AR9383 Sequence
AR9386 Cloning v
CQ866977 Sequence
AX478528 Sequence
AX478528 Sequence
AB116367 Expressio
AX768200 Sequence
AX768202 Sequence
AX768203 Sequence
AF140577 Integrati
AX431576 Sequence
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                                                                                                                                                                                                                            AR373251 Sequence
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                                                                                                                                                                                                                                                                                                                                            synthetic construct
synthetic construct
other sequences, artificial sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 3300;
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                AX202426
Sequence 14 from Patent W00152620.
                                                     AY219686
AY219688
AY219689
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AY219682
AY219683
AY219684
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AF177932
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Matches 3300; Conservative
1329.2
1238.4
1238.4
1237.2
1204
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i Dalmia, B. s expression in plants ; SYNGENTA AGRICULTURAL ruct"	/note="Partial sequence of pMal-m2 and zinc finger prote ZPPm2"  ZPPm2"  atch 100.0%; Score 3300; DB 6; Length 3300; and zinc finger protections.	Matches 3300; Conservative 0; Mismatches 0; Indel8 0; Gaps 0; Oy 1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGGTGCCCCGGAAGAGA 60	61 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG	121 GTGTCTTATCAGCGTTTCCCGCGTGGTGACCAGGCCAGCTTTTCTGCGAAAA  121 GTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGCCA	Db	301 ACGCGCCGTCGCAAATTGTCGCGCCGTTAAATTCTCGCGCCGATGACTGGCTGCCAGCCGCGAGCGGCGATTAAATTCTCGCGCCGATGACTGGCTGCCAGCGGGGGGGTTAAATTCTCGCGCCGAATTGTCTCGCGGCGGTTAAATTCTCGGGGCGATTAAATTCTCGGGGGGGG	361 TGGTGTGTGGATGGTAGAACGAAGCGGCGTCGAAGCCTGTAAAGCGGGGGGGG	421 TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 	Oy 481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA 540  Db 481 TTGCTGTGAAGCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTTGACCAGA 540	541	601	Oy 661 GGGTCTGGGTGGGTGGCTGGCATAAATATCTCACTGGCAATCAAT	Qy         721 CGGAACGCGACTGCACTGCCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA 780           Dh         721 CGGAACGCAAGGCCATGAAGTGCCATGCAAGTCCGGTTTTCAACAAACCATGCAATGCTGA 780	781 ATGAGGGCATCGTTCCCACTGCGATGCTGCCAACGATCAGATGGCGCTGGGCGCAA
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	AX202430 LOCUS LOCUS LOCUS DEFINITION Sequence 18 from Patent W00152620. AX202430 AX202430 AX202430 AX202430 AX202430 AX202430 KEYWORDS SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE SOURCE ORGANISM Synthetic construct ORGANISM Supthetic construct ORGANISM Substances; artificial sequences. THEFERENCE AUTHORS Barbas, C.F., Stege, J.T., Guan, X. and Dalmia, B. TITLE Methods and compositions to modulate expression in plants	AL Patent: WO 155820-A 18 26-JUL-2001; The Scripps Research Institute (US); SYNGENTA AGRICULTU DISCOVERY, INC. (CA) Location/Qualifiers 13300 urce /organism==synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="Parial sequence of pMal-Ap3 and zinc fin ZFPAp3"	Query Match         97.8%; Score 3226.4%         DB 6; Length 3300;           Best Local Similarity 98.6%; Pred. No. 0;         No. 0;           Matches 3254; Conservative 0; Mismatches 46; Indels 0; Gaps 0;           QY         1 CCGACACCAACGAAAACCTTTCGCGGTATGGCATGATAGGCCCGGAAGAG 60           Db         1 CCGACACCATCGATGGTGCAAAACCTTTCGCGGTATGGCATGATGCCCCGGAAGAG 60           QY         61 GTCAATTCGAGTGAAACCTTTTGCGGGTATGGCATGTAGAGGCCCGGAAGAGG 60           QY         61 GTCAATTCGAGTGAAACGTTATACGTTATACGATGTAGAGGTGCGAGGAAGCGCGAGGTATGCGCGAGGTATGCCGTATACGCTTATACGCTTATACGCTTATACGCTTATACGCAGGAGTATGCCG 120		241 241 301 301

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<pre>ORIGIN Query Match 97.4%; Score 3215.2; DB 6; Length 3300; Best Local Similarity 98.4%; Pred. No. 0; Matches 3247; Conservative 0; Mismatches 53; Indels 0; Gaps 0;</pre>	Qy         1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGGCCCCGGAAGAGA 60		181 CGCGGGAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC  181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC  181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC	QY         241 AACAACTGGCGGCAAACAGTCGTTGCTGATTGCGTTGCCAGTCTGGCCCTGC 300           DD         241 AACAACTGGCGGCGAAACAGTCGTTGCTGATTGCGGTTGCCACTCCAGTCTGGCCTGC 300           QY         301 ACGGCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTCCCAGC 360		421 TTCTCGGGCAACGCGTCAGTGGCTGATTAACTAACCGCTGGATGACGCGTGGTGGTGATGACTGATTAACTAAC	481 TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA	Oy 541 CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC 600	Qy 601 TGGTCGCATTGGGTCACCAGCAATCGCGCTGTTAGCGGGCCCCATTAAGTTCTGTCTCGG 660	Qy 661 CGCGTCTGCGTCTGGCTGGCCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 720	Qy 721 CGGAACGGGACTGGAGTGCCATGTCCGGTTTTCAACAAACCATGCAAATGCTGA 780 	Oy         781         ATGAGGGCATCGTACCGCGATGCTGCTTGCCAACGATCAGGGGCTGGGGCGCTGGGAA         840           Db         781         ATGAGGGCATCGTTCCCACTGGGATGCTGCTTGCTATCACGATGGGGTTGGCTTGGCTTGGCTTGGCTTGGCGTTGGCGTTGGTGTGGTG	841 TGCGCGCATTACCGAGTCCGGGCTTGCTTGCGATATCTCGGTAGTGGGTACGCGTACCGTTGCTTGC	901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 960 	Qy 961 GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1020

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961 GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA 1020 1021 AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAACAAAAAAAA		1141 CCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA	1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG 1260 	1261 TCAGGCAGCCATCGGAAGCTGTGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320 	1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTGCGCCGACATCATAACGGTT 1380 	1381 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440 	1441 ATTGTGAGGGAATATACACTCACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500	VTCTGG	1561 ATTAACGGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAATTCGAGAAAGAT 1620 	1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 		1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCGTAT 1800 	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 	1861 GAAGCGITATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920 	TCAAC			2041 TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100

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90 <b>%</b> 90	3 8 3 8 3 8	6 6 6 6 6	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	\$ 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	\$ 9 \$ 9 8	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	6 6 6 6 6
Db 2581 GCCAGCGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640  Qy 2641 AACAACAACAACAATAACAACAACACCCGGGATCGAGGATTTCAGAATTC 2700  Db 2641 AACAACAACAACAATAACAACAACAACACCTCGGGATCGAGGGAAGGATTTCAGAATTC 2700			Query Match     81.8%; Score 2698; DB 6; Length 9191;       Best Local Similarity 99.8%; Pred. No. 0;       Matches 2701; Conservative 0; Mismatches 5; Indels 0; Gaps 0;       Qy     1 CCGACACCATCGAATGGTGCAAAACCTTTCGGGGTATGGCATGATAGGGGAAGAGA 60       Dh     1 CCGACACCATCGAATGGTGAAAACTTTCGCGGTATGGCATGATAGGCAAGAGA 60	61 GTCAATTCAGGTGGTGAATGTGAACCAGTAACGTTATACGATGTGGCGGGTGTGGCGGGGTGTGGCGGGGGGGG		241 AACAACTGGCGGCGAAACAGTCGTTGCTGATTGGCGTTGCCACCTCCAGTCTGGCCCTGC 301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 301 TGGTGGTGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 361 TGGTGGTGTCGCAAATTGTCGCGGCGCTCCGAAGCCGGCGGTGCAAATC	Db 361 TGGTGGTGTCGATGGTAGAACGGGCTCGAAGCCTGTAAAGCGGGGTGCAATC 420  Qy 421 TTCTCGCGCAACGCTCAGTGGCTGATCATTAACTATCCGCTGGATGCCAGGATGCCA 480  L

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA circular SYN 28-JAN-2002 complete sequence.
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Sheffield, P.J., Garrard, S.M. and Derewenda, Z.S.
Direct Submission
Submitted (05-007-1998) Molecular Physiology and Biological
Physics, University of Virginia, 4215 Jordan Hall, 1300 Jefferson
Park Avenue, Charlottesville, Virginia 22908, USA
Location/Qualifiers
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1 (bases 1 to 6724).
Sheffield, P., Garrard, S. and Derewenda, Z.
Sheffield, P., Garrard, S. and Derewenda, Z.
Covercoming expression and purification problems of
family of 'parallel' expression vectors
Protein Expr. Purif. 15 (1), 34-39 (1999)
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TITLE
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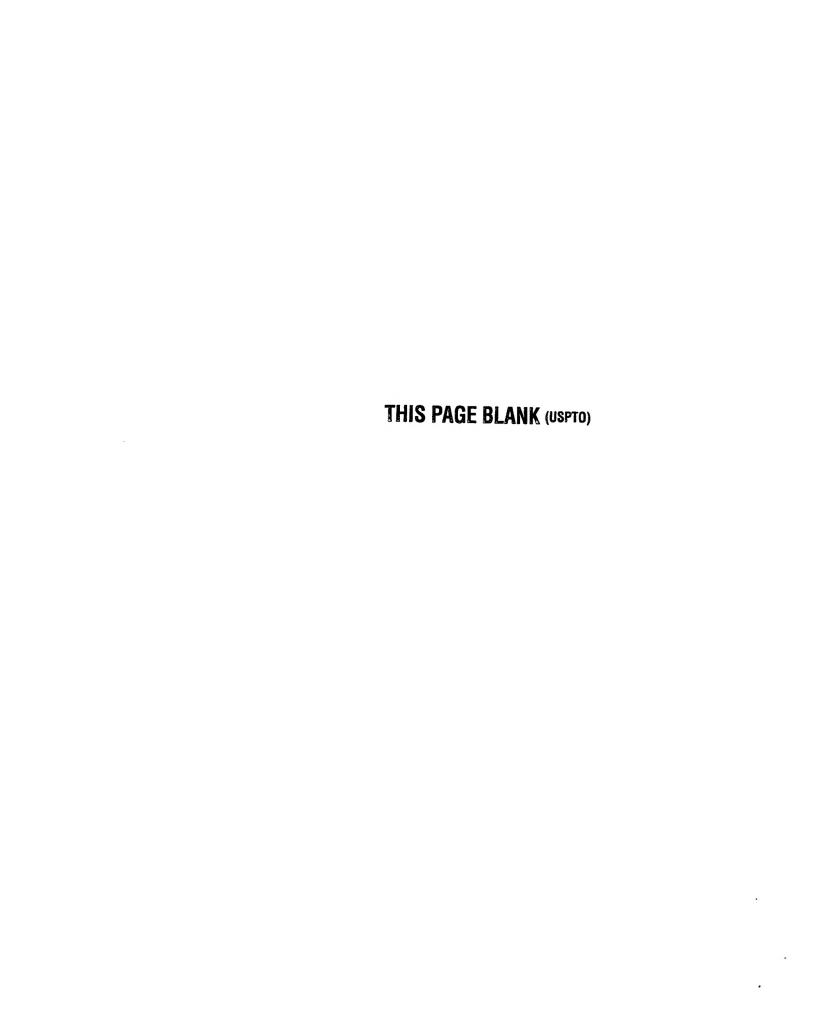
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                                                                                             90;
                                                        Length 6706;
                                                                                             Indels
                                                      DB 12;
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د
                                                    Score 2631; DE
Pred. No. 0;
0; Mismatches
                                               Query Match
Best Local Similarity 97.7%;
Matches 2704; Conservative
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                                                                                                                                                                                                              /codon_start=1
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GDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNT
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                    'notew"derived from commercially available vector pMal-p2
(New England Biolabs)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="M13 secretion signal sequence"
1582. .2973
/gene="malE-lacZa fusion"
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fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to include phage M13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="R-plasmid ampicillin resistance gene"
                                                                                                                                                                                                                                                                                                                                                                                                               /gene="lac1"
/note="transcriptional repressor"
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/Btandard_name="M13 origin (+ -)"
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transl_table=11
product="RTEM-1 beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1528. .1581
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xref="taxon:69327"
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                                                                             /gene="lacI"
/note="E. coli gene"
                                                                                                                    15. .46
/gene="lacI"
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Ad190419 Clostridi
Adf06053 Vector pJ
Ad173509 Plasmid p
Adh73509 Plasmid p
Adh73600 Plasmid p
Adh73600 Plasmid p
Adh73600 Plasmid p
Adh73600 E. coli t
Aav32977 Tn7 donor
Aad45059 Transposo
Ad466051 Plasmid p
Ad172229 DNA seque
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Ad60511 Plasmid p
Ad373099 MBP and z
Ad633532 Vector pl
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Zinc finger protein; ZFP; gene expression; metabolic pathway regulator; modulation; plant technology; agriculture; ds.
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note= "CDS does not include start and stop codon"
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1867. _2940
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'bound_moiety= "F2-f primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= a
product= "ZFPm4 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Partial sequence of pMal-m4 and ZFPm4 DNA.
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'bound_moiety= "Fl-f2
?770. .2850
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AD033532
AD033531
AAD29720
AAC55459
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824. .2889
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                                    ADH73599
ADH73598
ADH73600
ADH73601
ABZ23939
ABQ73200
AAV32977
AAD45059
ADC46817
ADL72229
ADL72229
ACF06051
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AAT90491
AD033522
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                                                                                                                                                                                             ADL18668
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2719. .3270
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/bound_moiety= "
2992. .3042
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 2916. . . . . . . . /*tag= f
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 *tag=
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1609.4
14652.4
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1418.2
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1238.4
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1237.2
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Aad11580 Partial 8
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Aah25681 Nucleotid
Aah25681 Nucleotid
Ad023608 DNA encod
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                                                                                        July 31, 2005, 14:24:04; Search time 1094.6 Seconds (without alignments) 17846.836 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the target gene.
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC
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Matches 3300; Conservative 0
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1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320 1321 TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT 1380 11111111111111111111111111111111111	CTGGCAA	ATTGTGAGGGGATAACAATTTGACAGGAAAAGGCGGCCGGTTTAGGTGTTTTGAGAAAAAGTGGAGGGGGGGG	GCACTTCACCAACAAGGACCATATATGAAAACTGAAGGAGGTAAACTAGTAATCTGG 	ATTAACGGCGATAAAGGCTATAACGGTCTCGCTCGAGGAAGAAGAATTCGAGAAAGATTTTTTTT	21 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT 		GCTCAATCTGGCCTGTTGGCTGAATCACCCGGACAAAGCGTTCCAGGACAAGCTGTAT 	CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATGGTGTT	GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA	GAGATCCCGGCGCTGGATAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC	CTGCAAGAACCGTACTTCACCTGGCCGGTGATTGCTGCTGGTGGGGGGTTATGCGTTCAAG 	TATGADACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 		2161 TCCATCGCAGAAGCTGCCTTTAATAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220 2161 TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220	2221 GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280	2281 AAGGGTCAACCATCCAAACCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCAGT 2340 	2341 CCGAACAAAGAGCTGGCAAAAGGTTCCTCGAAAACTATCTGCTGATGAGGTCTG 2400 

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New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of the target gene.
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bound_moiety= "F2-b primer"
867. _2940
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(SYGN ) SYNGENTA AGRIC DISCOVERY INC.
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2719. .3270
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/bound_moiety= "
7119, .3192
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3022. .3102
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2824. .2889
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3205. .3273
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/bound_moiety= "
3076. 3141
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/bound_moiety= "
3168. .3225
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2740. .2790
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21-JUL-2000; 2000US-00620897.
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P-PSDB; AAE06005.
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target of the zero sequence, where the expression of the target gene in the plant cells is modulated. The ZFP and fusions of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a giscultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-Ap3 (APETALA3) and ZFPAD3 DNA
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                                                                                                                                                                                                                                                                         98.0%; Score 3232.8; DB 4; Length 3300; 98.7%; Pred. No. 0; Live 0; Mismatches 42; Indels 0;
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                                                                                                                                                                                                                                                                                         Best Local Similarity 98.7
Matches 3258; Conservative
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Best Local S
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Example 4; Page 148-149; 156pp; English

GARGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAAAACCTGGAAAACCTGGAAAACCTGGAAAACCTGGAAAACCTGAAAACCTGAAAACCTGAAAACCTGAAAACCGAAAACCGAAAAACCTGAAAACCTGAAAACCGTGATTAACCGTTCAACGTTGAACCGTTGATTGA	2881 CTGGTGCGCCATCAACGCACTCATACTGGCGAGAAGCCATACAAATGTCCAGAATGTGC 2940 2941 AAGTCTTTCAGTGATTGTCGTGATCTTGCGAGGCACCAACGTACTCACACCGGGGAGAAG 3000
6 4 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8 6 8	g &
18   MICHOGOCOLTOCATCCACTCCACTCCACTCCACCACCACCACCACTCCACTCCACCCCCACTCCACCCCCACTCCACCCCCC	1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAAACCTGGGAA 1920

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Best Local Similarity 98.4 Matches 3247; Conservative
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               CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCTCAGAGCTCTCACCTGGTGCGCCAC 3060
                                                                                    CAGCGCCCCACCTGGAACGCCATCAACGCACTACTGGCGAGAAAGCCATACAAATGT 3180
                                                                                                         CCAGAATGTGGCAAGTCTTTCTCAACTTCAGGCCATTTGGTCCGTCACCAACGTACTCAC 3240
                                                                                                                      3181 CCAGAATGTGGCAAGTCTTTCTCAACTTCAGGCAACTTGGTCCGTCACCAACGTACTCAC 3240
                                                                                                                                        3241 ACCGGTAAAAACTAGTGGCCAGGCCGGCCAGTACCGGTACGACGTTCCGGACTACGCT 3300
2941 AAGTCTTTCAGCCAGTCCAGCAACCTGGTGCGCCACCAACGTACTCACACCGGGGAGAAG 3000
                                                                                                                                                  Zinc finger protein; ZFP; gene expression; metabolic pathway regulator; modulation; plant technology; agriculture; ds.
                                                            CAGCGTACCCACACGGTGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGC
                               CCCTATGCTTGTCCGGAATGTGGTAAGTCCTTCAGCACCAGTGGCTCCTTGGTTAGACAC
                                             CAGCGTACCCACACGGGTGAAAAACCGTATAAATGCCCAGAGTGCGGCAAATCTTTTAGC
                                                                            CGCAGCGATAACCTGGTGCGCCATCAACGCACTCATACTGGCGAGAAGCCATACAAATGT
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aaa:A1a)
aaa:H1s)
aaa:G1u)
aaa:G1u)
aaa:G2u)
aaa:A2y)
aaa:A2y)
aaa:A3y)
aaa:A3y)
aaa:A3y)
aaa:A3y)
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.2790,
.2793,
.2874,
.2880,
.2886,
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/bound moiety= "Fl-f2 primer"
2770. 2850
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2824. _2889
/*tag= d
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(pos:2875.
(pos:2875.
(pos:2878.
(pos:2884.
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(pos:3127.
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The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZPP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target nucleotide sequence, where the expression of the target gene in the plant cells is modulating or regulating gene expression of the ZFP proteins are useful for modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pMal-ml and ZFPml DNA
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                                                                                                                                                                                                                                                                                                                                                                           bound_moiety= "F4-f2 primer"
022. .3102
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'bound_moiety= "F4-f1 primer"
8076. .3141
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2953. .3021
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bound_moiety= "F2-b primer"
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bound moiety=
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21-JUL-2000; 2000US-00620897.
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P-PSDB; AAE06000.
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Gaps

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53; Indels

97.4%; Score 3215.2; 98.4%; Pred. No. 0; iive 0; Mismatches

DB 4; Length 3300;

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metabolic pathway regulator;
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                                                                                                                                                                                                                   /product= "ZFPm2 protein"
/note= "CDS does not include start and stop codon"
/partial
2740. .2790
/*tag= b
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/bound moiety= "F4-f1 primer"
3076. 3141
/*tag= j
/bound_moiety= "F5-b primer"
3119. 3192
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bound moiety= "F3-b1 primer"
953. 3021
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'bound_moiety= "F6-b2 primer"
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824. .2889
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bound_moiety= "F2-b primer"
867. _2940
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bound moiety= "F2-f primer"
916. _2973
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bound moiety= "F5-f primer"
168. 3225
                                                                                                                          Zinc finger protein; ZFP; gene expression; modulation; plant technology; agriculture;
                                                                                                    Partial sequence of pMal-m2 and ZFPm2 DNA.
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2719. .3270
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/bound_moiety= "
3205. .3273
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21-JUL-2000; 2000US-00620897.
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                                                               GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC
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                2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC
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2001-465325/50 P-PSDB; AAE06002 

The patent discloses methods and compositions to modulate the expression of a target gene in plant cells. The method involves providing plant cells with a zinc finger protein (ZFP) which is capable of specifically binding to a target nucleotide sequence or its complementary strand within a target gene and allowing the ZFP binding to the target molectide sequence, where the expression of the FPP proteins are useful or modulating or regulating gene expression and metabolic pathways in plants. The ZFP, fusion proteins and methods are useful in plant and agricultural technology. The method is useful particularly for treating a disorder in the plant cells, where the disorder is associated with abnormal expression of the target gene. The present DNA sequence is the partial sequence of pwal-m2 and ZFPM2 DNA New zinc finger proteins, useful for modulating or regulating gene expression and metabolic pathways in plants, e.g. for treating in the plant cells a disorder that is associated with abnormal expression of target gene. Example 4; Page 140-142; 156pp; English

Sequence 3300 BP; 847 A; 874 C; 876 G; 703 T; 0 U; 0 Other;

Gaps ; 0 DB 4; Length 3300; Indels 53; Score 3215.2; I Pred. No. 0; 0; Mismatches Query Match Best Local Similarity 98.4%; Matches 3247; Conservative ( Query

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120 120 9 GTCAATTCAGGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCGGAAGAGA cceacaccarcearidereceaaaccriricecegrarecearearaececceeaaeaea GTCAATTCAGGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG н 61 61

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TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA TTCTCGCGCAACGCGTCAGTGGCCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA 421 421

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DE Nucl 8 g S S 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 g 상음 8 6 8 8 8 8 1440 1620 1740 1860 1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTGGGCACACGACCGCTTTGGTGGCTTAC 1740 1920 1980 2040 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800 1920 2100 2100 2160 2160 2220 2220 2280 2340 2400 TOTOGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGACCGCTTTGGTGGCTAC TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG TGTCGCTCAAGGCGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCCGAAAAACCTGGGAA GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGGCCAAAAACCTGGGAA ATTAACGCCATAAAGGCTATAACGGTCTCGCTGAAGTCCGGTAAGAAATTCGAGAAAGAT ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAGAAATTCCCACAGGTT CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGCTGAGGGTTATGCGTTCAAG TCCATCGCAGAAGCTGCCTTTAATAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG TATGAAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG GGTCTGACCTTCCTGGTTGACCTGATTAAAACAAACACACATGAATGCAGACACCGATTAC TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2281 AAGGGTCAACCATCCAAACCGTTGGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCAGT AAGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCCAGGTATTAACGCCGCCAGT 1261

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Nucleotide sequence of human Cdc25C phosphatase DNA

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                  TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA
                                                                    TTGCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA
                                                                                                                   CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC
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                 protein, maltose binding protein; MBP; Cdc25C phosphatase;
1; Cdc25B2; Cdc25B3; cyclin-dependent kinase; CDK; cell division;
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iive 0; Mismatches
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                                                                                                                                                                                                                                                                                   (SCRC ) SCRAS SOC CONSEILS RECH
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30-MAY-2000; 2000FR-00006883.
21-SEP-2000; 2000FR-00012008.
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Cdc25C phosphatase, amine; Cdc25 phosphatase, spontaneous alopecia; alopecia; proliferative disease; parasitic disease; viral infection; neurodegenerative disease; myopathy; anglogenesis; psoriasis; restenosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents pMAL-HSCGC25C, a plasmid encoding human CGC25C phosphatase. The specification describes the use of arylbablatic secondary or tertiary amines for the production of medicaments for inhibiting CGC25 phosphatases, especially CGC25C phosphatases. The amines of the invention are used for treating poppatatases. The amines of the invention are used for treating radiation. They are also used for treating tumoural or non-tumoural proliferative diseases, parasitic diseases, viral infections, proliferative diseases are e.g. amplogeness, pronifections. They may are e.g. amplogeness, proliferation of mines are also useful for inhibiting the proliferation of microorganisms (especially yeasts) and in the treatment of all disorders conventionally treated with vitamin K or its derivatives
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/orte= "encodes maltose binding protein (MBP)"
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/note= "ORF of human Cdc25C"
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MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding MBP-ToxoP30de18(82-294aa) fusion protein.
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(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30de13C, Toxo30de12C and ToxoP30 MIX1 sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in mino acid sequence of Toxo30de13C P30 antigen sequence is substituted amino acid sequence of Toxo30de13C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-Toxo30de13C (S2-294aa) and MBP-ToxO30MIX1 fusion proteins. (I) is useful for detecting the presence of IGM antibodies to Toxo30de13C pand and processed sequence of IGM antibodies to Toxo30de13C pand detecting the presence of IGM antibodies with a composition comprising (I) and detecting the presence of (I)/IGM antibody complexes. The present sequence represents DNA encoding a MBP-moventy
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                                                                                     Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
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81.5%; Score 2690.4;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches
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TIGGEGGCATTGGGGGGAATGGGCGTGTTAGGGGGCCCATTAAGTTCTGTCTG	1561 ATTAACGGCGATAAAGGTCTCGCTGAAGTCGGTAAGAATTCGAGAAGT

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TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCTGTAAATCACTGCATAATTCG 1320
                                                                                           ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a purified P30 antigen (I) chosen from 3 fully amino acids added to the C-terminus of the amino acid sequences, having 1-6 moxo30del2C P30 antigen sequence, or comprising an amino acid sequence of roxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30del3C P30 antigen sequence cis substituted with alanine, or comprising the amino acid sequence chosen from MBP-Toxo30del3C(52-294aa) and MBP-ToxO30MIX1 entibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies contacting complexes. The presence of IgM antibody complexes. The present sequence represents of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-TOXO930 fusion protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo40del2C, Toxo50 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
                                                                              P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 S1.5%; Score 2690.4; DB 12; Length 7322; Similarity 99.8%; Pred. No. 0; A. Conservative 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 7322 BP; 1887 A; 1844 C; 1934 G; 1657 T; 0 U; 0 Other;
                                       DNA encoding MBP-ToxoP30dell0(52-284aa) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bliese TR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ginsburg SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Fig 25; 114pp; English
                                                                                                                                                                                                                                                                                                               02-OCT-2002; 2002US-00263153
                                                                                                                                                                                                                                                                                                                                                         02-OCT-2002; 2002US-00263153
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                            (MAIN/) MAINE G T.
(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maine GT, Patel CB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2004-304563/28.
                                                                                                                                                                 Toxoplasma gondii
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Matches 2694;
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	RESULT 10  AD021603 standard; DNA; 7352 BP.  XX AD021603; XX AD021603; XX AD021603; XX AD021603; XX AD021603; XX AD021603; XX YP TO-JUL_2004 (first entry) XX P30 antegen Toxo30del3C(52-294aa) fusion protein. XX YP TOxoplasma gondii, ds; gene. TOxoplasma gondii, ds; gene. TOxoplasma gondii. Synthetic. XX XX XX XX XX XX XX XX XX XX XX XX XX	
1321 TGTCGCTCAAGGGCACTCCCGTTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT   1380	1621 ACCGGANTTANAGTCACCGTTGAGCATCCGGANAACTCGGAAGAATTCCCACACGGTT 1680	

### 1.54; Score 2690.4; DB 12; Lengt Conservative 9.8; Pred. No. 0; Conservative 6, Mismatches 6, Indels CCGACACCATGATGGTGCAAAACCTTTGGGGTATGGCATGATGG GTCACTTCAGGGTGGAATGGTGAAAACCTTTGGGGTATGCGATGATGG GTCAATTCAGGGTGGAATGGTGAAAACCTTTGGGGTATACGATGTGG GTCAATTCAGGGTGGAATGGTGAAACCTTTGGGGTATACGATGTGG GTCAATTCAGGGTGGAATGGTGAAACCTTTGGGGTAATACGATGTGG GTCAATTCAGGGTGGAATGGTGAAACCTTTCCGGGCAGCCAGGCCAGG GTGGTCTTTATCAGACCGTTTCCGGGGTGGTGAATAACCTTCGGGCCAGGCCAGG GTGGTCTTTATCAGACCGTTTCCGGGGTGGTGAATAACTCCCAGGCAGG	with anti Toxo	with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-TOXOP30 fusion protein of the invention.	- Oy qo	961 GCCT      961 GCCT
CONTRICTION	- \$ X −	Score 2690.4; DB 12; Length 7352; Pred: No. 0; 0; Mismatches 6; Indels 0: Gans	ò 8	
CONTINUED   CONT		GAAAACCTTTGGGGGTATGGCATGATAGCGCCGGAAGAGA 60	o o	
COCCOCCADADACCACTICATACATATACATATACATATACATATACATATACATATACATATACATATACATATACATATACATATACATATACATACATATACATA		GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAAGTATGCCG	\$ 6	0-0
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COCCOMANANTICANGCOCCATCGCGAGCTCANTTACATTCCCAACCGCGTGCCACC   CIT		GTGTCTCTTATCAGACCGTTTCCCGCGTGGTGAACCAGGCCAGCCA	<u> </u>	9—v
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TGCGCGCCATTACCGAGTCCGGGCTGCGGATATCTCGGTAGTGGGATACG 900   QY 1981		TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGCGATACG	ý d	
ACGATACCGARGACAGGTCATGTTATATCCGCCGTTAACAACAGGATTTTC 960 ACGATACCGAAGACAGCTCATGTTATATCCCGCGTTAACAACAAGATTTTC 960 ACGATACCGAAGACAGCTATGTTATATCCCGCGTTAACCACCATCAACAAGATTTTC 960		TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGCTGCGGATATCTCGGTAGTGGGATACG	}	
		ACGATACCGAAGACAGGTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC	g 25	

CAATTCTCATGTTTGACAGCTTATCATCGACTGCACGGTGCACCAATGCTTCTGGCG GGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCG TTCACCAACAAGACCATAGATTATGAAAACTGAAGAAGGTAAACTGGTAATCTGG AATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT TTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT AAGAACCGTACTTCACCTGGCCGCTGATTCCTGCTGCTGACGGGGGTTATGCGTTCAAG TTACCTGGGATGCCGTACGTTACAACGCCAAGCTGATTGCTTACCCGATCGCTGTT

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The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30de13C, Toxo30de12C and Toxo930 MIXI sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30de13C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence consent from MBP-TOxo30de13C P30 antigen sequence chosen from MBP-TOxo30de13C(52-30da), MBP-TOxo30da14C(52-294a) and MBP-TOxO30MIXI fusion proteins. (I) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-TOxOP30 fusion protein of the invention.
                                                                                                                                                    Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIX1, useful for detecting presence of IgM or IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG
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99.8%; Pred. No. 0;
ive 0; Mismatches
                                             Bliese
                                             Ginsburg SR,
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                                                                                                                                                                                                                       antibodies to Toxoplasma gondii.
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Best Local Similarity 99.8
Matches 2694; Conservative
                                           Patel CB,
                                                                                       2004-304563/28
  (BLIE/) BLIESE T R.
                                                                                                              P-PSDB; ADO23599
                                           Maine GT,
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TATGAAAACGCCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG
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                                                                                       TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG
                                                                                                                                                                                                                                                                                                                                                                              P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding MBP-ToxoP30del3C(52-300aa) fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a purified P30 antigen (1) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIXI sequences, having 1-6 amino acids added to the C-terminus of the amino acid sequence of Toxo30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence of Toxo30del3C P30 antigen sequence is substituted with alanine, or comprising the amino acid sequence consent from MBP-Toxo30del3C(52-300aa), MBP-TOXO30del4C(52-294aa) and MBP-TOXO30MIXI fusion proteins. (1) is useful for detecting the presence of IgM antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (1) and detecting the presence of (1)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-TOXOP30 fusion protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo930 MIX1, useful for detecting presence of IgM or IgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
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                                                               P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 7370;
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                                DNA encoding MBP-ToxoP30MIX1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                         Ginsburg SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Fig 31; 114pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibodies to Toxoplasma gondii.
                                                                                                                                                                                                                                                                                               02-OCT-2002; 2002US-00263153
                                                                                                                                                                                                                                                             02-OCT-2002; 2002US-00263153
(first entry)
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PATEL C B.
GINSBURG S R.
BLIESE T R.
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                                                                                                                                       Toxoplasma gondii
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GAAGGGGTTAATAAAGACAGATGCGGTGGGGTGAAGGTCTTACGAGGAAGAG 2460		cc manno acids added to the C-terminus of the amino acid sequence of crox30de12C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the crox amino acid sequence of Toxo30de13C P30 antigen sequence is substituted comprising the amino acid sequence is substituted crox30de13C152-300aa), MBP-Toxo30de14C(52-294aa) and MBP-ToxO30de13C152-300aa).
1261   TCAGGCAGCCATCGGAAGCTGTGGCTATGCAGGTCGTAAATCACTGCATAATTCG   1320   1321   TGTCGCTCAAGGCGCACTCTGGATAATGTTTTTTGCGCCGACATCATAACGGTT   1380   1321   TGTCGCTCAAGGCGCACTCTCGGATAATGTTTTTTGCGCCGACATCATAACGGTT   1380   1321   TGTCGCTCAAGGCGCACTCTCGGATAATGTTTTTTGCCCCGACATCATAACGGTT   1380   1381   CTGGCAAATATTCTGAAGCGTTTGACATTAATCATCGGCTCGTATAATGTGTGGA   1440   1441   ATTGTGAGCGATAACAATTCACACGGAAACAATTAATCATCACGCTCGTTTAAGGTGTTTAACGG   1500   1441   ATTGTGAGCGATAACAATTCACACGGAAACAGCACACGCAACACGCCAGCTCGTTTAAGGTTTTCACA   1500   1501   GCACTTCACCAACAACAACACACACAGGAAACACGCCAGCAAACACGCCAGTAACTGCGTAAATTCTGG   1500   1501   GCACTTCACCAACAAGAACAATAATAACGGCGATAAACGGCCAATAAAACTGAAAACTGGAAAACTGGTAAATCTGG   1501   ATTAACGGCGAATAAACGGCTATAACGACCGAAAAACACGCCAATAAACGACCGAAAAAACAGACCTCACAAAAAACAACAACAAAAAAAA	1621   ACCGGANTTAAAGTCACCGTTGAGCATCACATAACTGGAAGAAATTCCCACAGGTT 1620   1621   ACCGGANTTAAAGTCACCGTTGAGCATCCGGATAACTGGAAGAAATTCCACAGAGTT 1680   1681   GCGGCAACTGGCCTGGCCTTGATGATTCTCTCGGGACCACACGCTTGTT 1680   1681   GCGCCACTGGCCTGGCCTGTTGATGCTTCTGGGCCACACACGCTTGTT 1800   1741   GCTCAATCTGGCCTGATTAACTCTCCCGGAAAACGCTTCACGCACAGCTGTTT 1800   1741   GCTCAATCTGGCTGATTAACTCCCCGGAAAACGCTTCAAGTCTGTTTA 1800   1741   GCTCAATCTGGCTGATTAACACCTGAAATCACCCCGGAAAAACGTTAACCTGTTTA 1800   1801   CCGTTTAACTGGGTGATTAACACGCAAAACGCTGAATTAACACACATAACACGCTAACTGCTTAACCTGGATGATTAACACGAAAACGCTGAATTAACACAGAATTCTGCTGCCCGAACACCTGCTTT 1800   1921   GAAGCGTTAACCGGAAAAACCTGAAAACGCAAAAACGCAAAAACCTGAAAACGAAAATTCAACACAAAATCTGCTGCCCCAAAAACCTGCAAAAACGCAAAAACGCAAAAAATTAACAAAAATTAAAAAAAA	2281 AAGGTCAACCATCCAAACCGTTCGTTGGCGTGCTCAGCGCAGGTATTAACGCCGCCAGT 2340 2341 CCGAACAAAGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTG 2400 2341 CCGAACAAAGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTG 2400 2341 CCGAACAAAGAGTTCCTCGAAAACTATCTGCTGACTGATGAAGGTCTG 2400

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antibodies to Toxoplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-Toxop30 fusion protein of the invention.
                                                                                                                                         GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG
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encoding MBP-ToxoP30MIX3 fusion protein. 01-JUL-2004 (first entry) ADO23644;

P30 antigen, Toxo30del3C; Toxo30del2C; ToxoP30 MIX1; MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1; Toxoplasma gondii; ds; gene.

Toxoplasma gondii Synthetic

US2004067239-A1.

08-APR-2004

02-OCT-2002; 2002US-00263153

02-OCT-2002; 2002US-00263153

(MAIN/) MAINE G T.

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                                                                                      Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo50del2C, Toxob30 MIX1, useful for detecting presence of IgM or IgG antibodies to Toxoplasma gondii.
                                                                                                                                                                                                                                                                                                                                                                      CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCGGAAGAGA
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                                                                                                                                                                                                                                                                                                            Sequence 7370 BP; 1900 A; 1857 C; 1950 G; 1663 T; 0 U; 0 Other;
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                                          Bliese TR;
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99.8%; Pred. No. 0;
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                                         Ginsburg SR,
                                                                                                                                        Example 5; Fig 33; 114pp; English.
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(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
                                        Patel CB,
                                                          2004-304563/28.
                                                                     P-PSDB; ADO23645
                                      Maine GT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a purified P30 antigen (I) chosen from 3 fully defined Toxo30del3C, Toxo30del2C and ToxoP30 MIXI sequences, having 1-6 amino acids acids added to the C-terminus of the amino acid sequence of ToxO30del2C P30 antigen sequence, or comprising an amino acid sequence in which at least one of the five C-terminal cysteine amino acids of the amino acid sequence is substituted with alanine, or comprising the amino acid sequence is substituted with alanine, or comprising the amino acid sequence chosen from MBP-TOXO30del3C (52-230aa), MBP-TOXO30del4C (52-294aa) and MBP-TOXO30MIXI fusion proteins. (I) is useful for detecting the presence of IgM antibodies to ToxOplasma gondii in a test sample, which involves contacting the test sample suspected of containing the IgM antibodies with a composition comprising (I) and detecting the presence of (I)/IgM antibody complexes. The present sequence represents DNA encoding a MBP-CXC TOXOP30 fusion protein of the invention.
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                                                                                                                                                                                                 P30 antigen; Toxo30del3C; Toxo30del2C; ToxoP30 MIX1;
MBP-Toxo30del3C(52-300aa); MBP-Toxo30del4C(52-294aa); MBP-Toxo30MIX1;
Toxoplasma gondii; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel purified polypeptide having sequence identity to amino acid sequence of P30 antigen of Toxoplasma gondii e.g. Toxo30del3C, Toxo30del2C, ToxoP30 MIXI, useful for detecting presence of IgM or antibodies to Toxoplasma gondii.
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81.5%; Score 2690.4; DB 12; Length 7403;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches 6; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7403 BP; 1907 A; 1863 C; 1961 G; 1672 T; 0 U; 0 Other;
                                                                                                                                                     DNA encoding MBP-ToxoP30del2(52-311aa) fusion protein
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                             DNA; 7403
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                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MAIN/) MAINE G T.
(PATE/) PATEL C B.
(GINS/) GINSBURG S R.
(BLIE/) BLIESE T R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-304563/28.
P-PSDB; ADO23595.
                         ADO23594 standard;
                                                                                                                                                                                                                                                                                        Toxoplasma gondii
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                                                                                                                                                                                                                                                                                                                  Synthetic
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	Search completed: August 1, 2005, 04:28:52 Job time : 1102.6 secs					
1261 TCAGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGATAATTCG   1320	ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTTACGGAATTAAAGTCACCACAGGTTACGGAATTAAAGTCACCGAATTAAAGTCACGGAATTAAAGTCACCGATTCAGAGTTCCGAAGTTTCCCACAGGTTGCGAAATTAAAGTCACCGAATTAAAATTCCACAGGTTGGAAGAAAAAAAA	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800  1741 GCTCAATCTGGCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800  1801 CCGTTTACCTGGGATGCCGTACGTTACACGGCAAGCTGATTACCTTACCCGATCGCTGTT 1860  1801 CCGTTTACCTGGGATGCCGTACGTTACACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860  1801 CCGTTTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCGATCGCTGTT 1860	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAAACCTGGGAA 1920	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGTTATGCGTTCAAG 2040		

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COUNTRY: U.S.A.
ZIP: 07110
STREET: 340 K.
CITY: Nutley
STATE: N.J.
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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-702-705-785

US-09-71-125-785

US-09-671-125-785

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US-09-671-125-785

US-09-65-417-185

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RESULT 1

US-08-91-03-1

US-08-91-03-1

Sequence 1. Application US/08971036

| Sequence 1. Application US/08971036
| Sequence 1. Application US/08971036
| GENERAL INFORMATION: Michael R APPLICANT: Allow, Parid N APPLICANT: Asy, Parid N APPLICANT: Asy, Parid N APPLICANT: Way, Parid N APPLICANT: Way, Parid N APPLICANT: Wilson, Parid N APPLICANT: Wilson, Parid N APPLICANT: Wilson, Parid N APPLICANT: Wilson, Parid N APPLICANT: US-A. ADDRESSE: Hoffmann-La Roche Inc.

OTTY: While OF INVERTION: Maino Acid Derivatives

NUMBER OF SEQUENCE: Sequence: ADDRESS: STREET: 30 (Kingeland Street

OTTY: While N APPLICANT: US-A.

OCHUTER: N-1.

COMPUTE: REARABLE FORM:

MEDIUM TYPE: PLODY MICHAEL PORM:

MEDIUM TYPE: PLODY MICHAEL PORM:

MEDIUM TYPE: PLODY MICHAEL PORM:

MEDIUM TYPE: PLODY MICHAEL PORM:

MEDIUM TYPE: PLODY MICHAEL PORM:

MARIE TRANDERS: Parent'IN Release #1.0, Version #1.25

CLASSIFICATION: WINNER: 1887 Compatible

MANG: PRESENTATION NUMBER: 1882

MANG: PRESENTATION NUMBER: 1882

MANG: PRESENTATION NUMBER: 1882

MEREPRESENTATION NUMBER: 1882

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61 GTCAATTCAGGGTGGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120 	ò a	1141 CCCGACTGGAAAGCGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCTCACTCA
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181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCAACCGCGTGGCAC 240	දු දු	1261 TCAGGCAGCCATCGGAAGCTGTGGCTGTGCAGGCGTCGTAAATCACTGCATAATTCG 1320 
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301 ACGCGCCGTCGCAAATTGTCGCGGCGATTAAATCTCGCGCCGATCAACTGGGTGCCAGCG 360 	ò a	1381 CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA 1440 
CAATC 4	à a	1441 ATTGTGAGCGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 
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REFERENCE/DOCKET NUMBER: RAN 4430/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (973) 235-2363
TELEFAX: (973) 235-2363
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7475 base pairs
LENGTH: 7475 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                              81.8%; Score 2700; I
100.0%; Pred. No. 0;
Live 0; Mismatches
                                                                                                                                                TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Best Local Similarity
Matches 2700; Conservat
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COUNTRY: U.S.A.

ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.
APPLICATION NUMBER: US/09/096,570
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Attwood, Michael R
APPLICANT: Hurst, David N
APPLICANT: Hurst, David N
APPLICANT: Fary, Paul B
APPLICANT: Raynham, Tony M
APPLICANT: Wilson, Francis X
TITLE OF INVENTION: Amino Acid Derivatives NUMBER OF SEQUENCES: 2
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/971,036
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-096-570-1; Sequence 1, Application US/09096570; Patent No. 6018020; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 38522
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     GCCTGCTGGGGGCAAACCAGGGGGGCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
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                                      GCCTGCTGGGGCAAACCAGCGTGGACCGCTTGCTGCAACTCTCTCAGGGCCAGGCGGTGA
                                                                               AGGGCAATCAGCTGTTGCCCGTCTCACTGGTGAAAAGAAAAACCACCCTGGCGCCCCAATA
                                                                                                                        CGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTGGCACGACAGGTTT
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                                                                                                                                             CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA
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                                                                                                                                  CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCGGAAGAGA
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i LENGTH: 7475
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FRATURE:
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TOPOLOGY: circular
WOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "pEM delta R.adj to 1"
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43.0%; Score 1417.6;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 1455; Conservative 0; Mismatches
NAME: Brown, Anne
REGISTRATION NUMBER: 36,463
REPERENCE/CDCKET NUMBER: 5789-3
TELECOMMULICATION INFORMATION:
TELEPHONE: 919 420 2205
TELEPAX: 919 881 3175
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5926 base pairs
TYPE: nucleic acid
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| Patent No. 6420524
| GENERAL INFORMATION: APPLICANT CRAIG NANCY L. TITLE OF INVENTION: ATP-DEPENDENT TRANSPOSITION PROTEINS | TITLE OF INVENTION: ATP-DEPENDENT TRANSPOSITION PROTEINS | NUMBER OF SEQUENCES. 15 | CORRESPONDENCE ADDRESS: ADDRESSE: Anne Brown (Alston & Bird, LLP) | STREET: ASOS Glenwood Ave. | STREET: ASOS Glenwood Ave. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREET: NC. | STREE
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COMPUTER REABBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/027,169
FILING DATE:
FLING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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 Length 5201;
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 DB 4;
Score 1362; DB Pred. No. 0; Mismatches
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Query Match
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Matches 1380; Conserv
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Facent No. 6720142
Facent No. 6720142
GENERAL INFORMATION:
FAIL SEQUENCE 3. APPLICANT: Hall, Barry G.
TITLE OF INVENTION:
FILE OF INVENTION: RESISTANCE GENES AND USE THEREOF TO SCREEN FOR DRUG
TITLE OF INVENTION: FEFFICACY
TITLE OF INVENTION: FEFFICACY
TITLE OF INVENTION: FEFFICACY
TITLE OF INVENTION: FEFFICACY
TITLE OF INVENTION: FEFFICACY
TITLE OF INVENTION: FEFFICACY
TITLE OF INVENTION UNMBER: US/09/640,882
CURRENT APPLICATION NUMBER: G0/149,813
FRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 5201
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               GAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATG
                                       CCCCCATTACCGAGTCCGGCCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGAC
                                                        664 GATACCGAAGACAGCTCATGTTATATCCCGCCGTCAACCACCATCAAACAGGATTTTCGC
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CRGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence:
COTHER INFORMATION: pACSE2
US-09-640-882-2
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| Patent No. 6720142
| Patent No. 6720142
| GENERAL INFORMATION:
| APPLICANT: Hall, Barry G. | ITLE OF INVENTION: RESISTANCE GENES AND USE THEREOF TO SCREEN FOR DRUG TITLE OF INVENTION: RESISTANCE GENES AND USE THEREOF TO SCREEN FOR DRUG TITLE OF INVENTION: BFFICANT | ITLE OF INVENTION: BFFICANT | ITLE OF INVENTION: BFFICANT | ITLE OF INVENTION: BFFICANT | ITLE OF INVENTION: BFFICANT | ITLE OF INVENTION: BFFICANT | ITLE OF INVENTION: BFFICANT | ITLE OF INVENTION NUMBER: US/09/640,882 | CURRENT FILING DATE: 2000-08-18 | PRIOR FILING DATE: 1999-08-19 | NUMBER OF SEQ ID NOS: 17 | SOFTWARE: Patentin Ver. 2.1 | SEQ ID NO 3 | LENGTH: 5201
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AGGCAGCCATCGGAAGCTGTGGTATGGCTGTGCAGGTCGTAAATCACTGCATAATTCGTG 1322
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99.1%; Pred. No. 0;
tive 0; Mismatches 10; Indels 2
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ORGANISM: Artificial Sequence
PEATURE:
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Best Local Similarity 99.11
Matches 1380; Conservative
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APPLICANT: UENO, EIICHI
APPLICANT: UENO, EIICHI
APPLICANT: OXADA, MASAHISA
TITLE OF INVENTION: EXPRESSED FROM SAID FUSED DNA SEQUENCE AND METHOD FOR TITLE OF INVENTION: EXPRESSED FROM SAID DNA SEQUENCE AND METHOD FOR TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE AND METHOD FOR TITLE OF INVENTION: EXPRESSING SAID DNA SEQUENCE
CORRESPONDENCE ADDRESSE:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
                   2243
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STRAIN: BL21 (DE3)
FUBLICATION INFORMATION:
AUTHORS: NOBUVUKI FUJII ET AL,
TITLE: FUSED DNA SEQUENCE, FUSED PROTEIN EXPRESSED
TITLE: FROM SAID FUSED DNA SEQUENCE AND METHOD OF
TITLE: EXPRESSING SAID FUSED PROTEIN
RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 4557
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,717
FILING DATE: 12-DEC-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 352225/1995
FILING DATE: 28-DEC-1995
ATTOCNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN P.
REGISTRATION NUMBER: 24,618
REFENCE/DOCKET NUMBER: 2084-031-0
TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
ORIGINAL SOURCE:
                                                                                                                                   RESULT 7
US-08-778-717-5
; Sequence 5, Application US/08778717
? Betent No. 6602689
; GENERAL INFORMATION:
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TELEPHONE: 703-413-2220
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
                                                1383 GGCAAATATTCT 1394
                                                                     Matches 1204; Conservative
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US-08-487-283A-18/c
Sequence 18, Application US/08487283A
Patent No. 6355245
GENERAL INFORMATION:
APPLICANT: Evans, Mark J.
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                                                                                                                     Sequence 2, Application US/08148675A
| Patent No. 5506121
| GENERAL INFORMATION:
| APPLICANT: Skerra, Arne; Schmidt, Thomas
| TITLE OF INVENTION: STREPTAVIDIN
| TITLE OF INVENTION: STREPTAVIDIN
| TORRESPONDENCE ADDRESS:
| ADDRESSE: Felfe & Lynch
| STREET: 805 Third Avenue
| CITY: New York City
| COUNTRY: USA
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99.8%; Pred. No. 0;
tive 0; Mismatches
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3832 bases
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Best Local Similarity 99.8
Matches 1202; Conservative
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STRANDEDNESS: single
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US-08-148-675A-2
                                     GCAC 1204
                                                            GCAC 3766
                                                                                                RESULT 8
US-08-148-675A-2
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Lenardo. Michael J.
McFarland, Henry F.
Matis, Louis A.
Mueller, Eileen Elliott
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Sequence 21, Application PC/TUS9605611A

GENERAL INFORMATION:
APPLICANT: Mueller, John P.
APPLICANT: Lenardo. Michael J.
APPLICANT: Meriand, Henry F.
APPLICANT: Matis, Louis A.
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APPLICANT: Matis, Louis A.
APPLICANT: Mueller, Eileen Elliott
APPLICANT: Nye, Steven H.
APPLICANT: Nother, Russell P.
APPLICANT: Rother, Russell P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Thomas, Thomas C.
APPLICANT: Thomas, Thomas C.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: OF INFLAMMATORY DISEASES
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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MOLECULE TYPE: Other nucleic acid
DESCRIPTION: DET Trc SO5/NI
DESCRIPTION: prokaryotic expression vector
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.4Mb storage
COMPUTER: Macintosh Cetris 610
CORPUTER: Macintosh Cetris 610
CORFWATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,283A
FILING DATE: June 7, 1995
PRIOR APPLICATION NUMBER: US 08/236,208
FILING DATE: 02-MAY-1994
ATTORNEY AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (203)772-3655
INFORMATION FOR SEQ 1D NO: 18:
SEQUENCE CHARACTERISTICS:
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99.8%; Pred. No. 0;
ative 0; Mismatches
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STREET: 25 Science Park (Alexion)
CITY: New Haven
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TYPE: Nucleic Acid
STRANDEDNESS: Double
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: USA
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COUNTRY:
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US-10-263-103-35/C
; Sequence 35, Application US/10263103
; Patent No. 6821723
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PASTEUR
; APPLICANT: Chevalier, Michel
; APPLICANT: El Habib, Raphaelle
; APPLICANT: Krell, Tino
; APPLICANT: Sodoyer, Regis
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APPLICANT: Nye, Steven H.
APPLICANT: Pelfrey, Clara M.
APPLICANT: Squinto, Stephen P.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: Modified Myelin Protein Molecules
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSES: Maurice M. Klee
STREET: 1951 Bur Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prokaryotic expression vector
                                                                                                                                                                                                                                                                                               COMPUTER: Macinicom, Control Computers: Microsoft Word 6.0.1
SOFTWARE: Microsoft Word 6.0.1
CURRENT APPLICATION DATA:
PELING DATE: 02-MAY-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/431,644
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/431,648
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: May 2, 1995
APPLICATION NUMBER: 08/482,114
FILING DATE: May 2, 1995
APPLICATION NUMBER: 30,399
REGISTRATION NUMBER: 30,399
REFERENCE/OCKET NUMBER: 30,399
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFRAX: (203) 254 1101
INPORMATION FOR SEQ 1D NO: 21:
GEOVIENCE
                                                                                                                                                                                                                                                COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 0.8 Mb storage
COMPUTER: Macintosh Centris 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Circular
MOLBCULE TYPE: Other nucleic acid
DESCRIPTION: DET Trc SOS/NI
DESCRIPTION: prokaryotic expres
                                                                                                                                   ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
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TYPE: Nucleic Acid
STRANDEDNESS: Double
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Best Local Similarity
Matches 1201; Conserv
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                      TGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACG
                                                                                                                           ACGATACCGGAGGCAGCTCATGTTATATCCCGCCGTTAAACCACCATCAAACAGGATTTTC
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                                                                                                     ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC
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Sequence 1, Application US/08929967

Patent No. 5891637

GENERAL INFORMATION:

APPLICANT: Ruppert, Siegfried J.W.

TITLE OF INVENTION: Construction of Full-Length cDNA Libraries

TUTLE OF INVENTION: Construction of Full-Length cDNA Libraries

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMBUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfratin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.3%; Score 1199.2;
99.8%; Pred. No. 0;
tive 0; Mismatches
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REPERRINCE/DOCKET NUMBER: P103;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-3216
TELEFAX: 650/952-9881
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity 99.8
Matches 1201; Conservative
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TITLE OF INVENTION: gp41 antigen
FILE REFERENCE: 01-1692-A
CURRENT APPLICATION NUMBER: US/10/263,103
CURRENT FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
SEQ ID NO 35
LENGTH: 5312
                                                                                                                                                                                                                  ) OTHER INFORMATION: plasmid per-cer
US-10-263-103-35
                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial
FEATURE:
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	RESULT 13 US-09-702-705-785/C  is Sequence 785, Application US/09702705  is Patent No. 6504010  is GENERAL INPORMATION:  is APPLICANT: Wang, Tongtong  is APPLICANT: Bangur, Chaitanya S.  APPLICANT: Panger, Gary  is APPLICANT: Panger, Gary  APPLICANT: Panger, Gary  APPLICANT: Panger, Darrick  APPLICANT: Retter, Marc  APPLICANT: Retter, Marc  APPLICANT: Retter, Marc  APPLICANT: Retter, Marc  APPLICANT: Retter, Marc  ITILE OF INVENTION: DAGNOSITIONS AND METHODS FOR THE THERAPY AND  TITLE OF INVENTION: DAGNOSITIONS OF LUNG CANCER  FILE REFERENCE: 210121.478614  CURRENT APPLICATION NUMBER: US/09/702,705  CURRENT FILING DATE: 2000-10-30  NUMBER OF SEQ ID NOS: 1833  SOFTWARE: FastSEQ for Windows Version 3.0  LENGTH: 5502  TYPE: DNA  IGAGLIANS HOMO SEDIEN	Ouery Match  Best Local Similarity 99.8%; Score 1199.2; DB 4; Length 5502;  Best Local Similarity 99.8%; Score 1199.2; DB 4; Length 5502;  Best Local Similarity 99.8%; Score 1199.2; DB 4; Length 5502;  Matches 1201; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  Oy 1 CCGACACCATCGAATGGCAAAACCTTTCGCGGTATGGCATGATAGGCCCGGAAGAGA 4618  Oy 617 GGGACCCTTCGAATGGGAAAACTTCGCGGTATGGCATGATGGCCCGGAAGAGA 4618  Oy 121 GTGATTCAGGTGGTGAAAACTTCCGCGTGAACGTTATACGATGTCGCAGGTATGCCG 120  Db 4617 GTCAATTCAGGCTGAAAGCTGAAACCTTATACGATGTCGCAGGTATGCCG 4558  Oy 121 GTGTCTCTTATCAGACGTTCCGGCGTGAAACCTTATACGATGTCGCAGGTTATCCGAAAA 4498  Oy 122 GTGTCTCTTATCAGACGTTCCGGCGGGGGAACCAGGCCAGGCTTCTGCGAAAA 4498  Oy 124 GTGTCTCTTATCAGACCGTTCCCGGGGGGAACCAGGTTTCTGCGAAAA 4498  Oy 125 GTGTCTCTTATCAGACCGTTCCCGGGGGGGAACCAGGTTTCTGCGAAAA 4498  Oy 126 GTGTCTCTTATCAGACCGTTCCGGGGGGAACCAGGCCAGCAGGTTGCCAGGTTGCAGGGGAAAAACTGGGGGAAAAACTGGGGGGGAAACTGGGGGGGAACTTATACATTCCCAACCGGTGGCAAAA 4498  Oy 127 GGCGGGAAAAAGTGGAAGCGGCGATGGGGGGGGGGGGGG
CCGACACCATCGAATGGTGCAAAACCTTTGGCGGTATGGCATGATAGCGCCCGGAAGAG 60		4270 CACCCATCAACATATATTTCCCCATGAACACGATCGCACTGGCCTGCACTGCCTCTC 4211 601 TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 660 4210 TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 4151 661 CGCGTCTGGCTGGCTGGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG 4151 661 CGCGTCTGGCTGGCTGGCAAAATTGTCACTCGCATCAAATTCAGCCGATAG 720 4150 CGCGTCTGGCTGGCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAG 4091 721 CGGAACGGGAACGGCATGGAGTGCCATGCTGCTTTTCACAAATTCAGCCGATAG 4091 721 CGGAACGGGAACGGCATGGAGTGCCATGTCGCGTTTTCAACAAATTCAGCCGATAG 4091 721 CGGAACGGGAACGGCATGGAGTGCCATGTTTTCACAAAATTCAGCCAATGCTGA 4091 721 CGGAACGGGAACGGCATGGAGTGCCATGTTTTCAACAAACCATGCCAATAGTTGA 4091 721 TGGGGGAACGGGAACGGCATGGTGCTGGTTTTCAACAAACCATGCCGATAG 4091 722 CGGAACGGGAACGGGATGCTGGTTGCTCGCAATTTCACAAAATGCTGA 4091 723 ATGAGGGAATCGTTCCCCACTGCTGTTTTCAACAAACAAA

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                                                                                                          Length 5502;
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                                                                                                                             3; Indels
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Pred. No. 0;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SEQ ID NO 785
LENGTH: 5502
                                                                                                        Query Match
Best Local Similarity 99.8%;
Matches 1201; Conservative C
                                                            TYPE: DNA
CORGANISM: Homo sapien
US-09-736-457-785
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                                                                        TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGG
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Job time: 356.4 secs
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APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Tongtong
APPLICANT: Fanger, Tom
APPLICANT: Panger, Tom
APPLICANT: Carter, Darrick
APPLICANT: Rannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: 12478
TITLE OF SINCENT APPLICATION NUMBER: US/09/614,124B
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT APPLICATION NUMBER: US/09/614,124B
SOFTWARE: FactSQ for Windows Version 3.0
SEQ ID NO 785
LENGTH: 5502
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Pred. No. 0;
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// Patent No. 6630574
// GENERAL INFORMATION:
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Best Local Similarity 99.8%;
Matches 1201; Conservative C
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US-09-614-124B-785
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US-09-765-555-17
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                    US-10-343-859-9

US-10-263-153-40

US-10-263-153-35

US-10-263-153-25

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US-10-263-153-61

US-10-263-153-61

US-10-263-153-15

US-10-263-153-15

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ive 0; Mismatches
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  Sequence 18, Appl
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Sequence 16, Appl
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Sequence 5, Appli
                                                                                                                                                                   Search time 1309.2 Seconds (without alignments)
16314.373 Million cell updates/sec
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| Cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
| Cgn2_6/ptodata/1/pubna/USO0_PUBCOMB.seq:*
                            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-765-555-18
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US-09-765-555-16
US-10-257-384A-1
US-10-149-472-5
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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Sequence 54, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 30, Appli Sequence 3, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli

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US-09-765-555-18
                                                                                                                               APPLICANT: The Scripps Research Institute
ITTLE OF INVENTION: Methods and compositions to modulate;
ITTLE OF INVENTION: expression in plants
ITILE OF INVENTION: expression in plants
FILE REFERENCE: 27801-20014.40
CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT APPLICATION NUMBER: US 09/620,897
PRIOR APPLICATION NUMBER: US 09/620,897
PRIOR APPLICATION NUMBER: US 00/177,468
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 00/177,468
PRIOR SELING DATE: 2000-01-21
SROFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.0%; Score 3232.8; Best Local Similarity 98.7%; Pred. No. 0; Matches 3258; Conservative 0; Mismatches
                                                     US-09-765-555-18

US-09-765-555-18

Sequence 18, Application US/09765555

Publication No. US20030037355A1

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
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1201 GCACAATTCTCATGTTTGACAGCTTATCATCGACTGCACCGATGCTTCTGGCG   1260   1261   TCAGGCAGCCATCGAAGCTGTGGTATGGCTGCAGGTCGTAAATCTCG   1320	CACGA 150 CACGA 150 CACGA 150 ICTGG 156 ICTGG 156 ICTGG 156 ICTGG 156			1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGACCGCGCTGATGTTCAAC 1980  1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980  1981 CTGCAAGAACCGTACTTCACCTGGCGCTGATTGCTGCTGCAGCGCTGATGTTCAAC 1980  1981 CTGCAAGAACCGTACTTCACCTGGCGCTGATTGCTGCTGAGGGGTTATGCGTTCAAG 2040  2041 TATGAAAACGGCAAGTACGACCGCTGATTACTGCTGCTGAGGGGGTTATGCGTTCAAG 2040  2041 TATGAAAACGGCAAGTACGACCATTAAAGACGTGGCGCGGAAAGCG 2100	2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAACAACACTGAGTGACGCTGGCGGAAAGCG 2100 2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACTGAATGAA	2221 GCATGGTCCAACATCGACCAGCAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280 2221 GCATGGTCCAACATCGACACCAGCAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280 2221 AAGGGTCAACATCCCAAACGTTCGTTGGTCGTGGCCAGGTATTAACGCCCAGCAGT 2340 [

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98.4%; Pred. No. 0;
ive 0; Mismatches
TITLE OF INVENTION: expression in plants
CURRENT APPLICATION NUMBER: US/09/765,555
CURRENT FILING DATE: 2002-05-24
PRIOR APPLICATION NUMBER: US 09/620,897
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 60/177,468
PRIOR PRIOR DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 75
SEQ ID NO 15
LENGTH: 3300
                                                                                                                                                                       OTHER INFORMATION: Partial sequence of OTHER INFORMATION: protein ZFPm2
                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                          Conservative
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Matches 3247; Conserv
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NAME/KEY: CDS
LOCATION: (1528)..(3453)
OTHER INFORMATION: /product = fusion protein MBP Cystatin C BMP-2
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DATABASE ENTRY DATE: 2001-05-07
RELEVANT RESIDUES: 1528 - 3453
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                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 1, Application US/10257384A
Publication No. US20040087524A1
Publication No. US20040087524A1
GENERAL INFORMATION:
TITLE OF INVERTION:
TITLE OF INVERTION:
TITLE OF INVERTION:
CURRENT APPLICATION NUMBER: US/10/257,384A
CURRENT FILING DATE: 2003-08-21
FRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2000-04-18

PRIOR FILING DATE: 2000-04-18

NUMBER OF SEQ ID NOS: 19

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        TIGCTGIGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTTCTTGATGTCTCTGACCAGA 540
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                                                                             CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGGCGTGCATC
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                                                  CACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGACTGGGCGTGGAGCATC
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US-10-149-472-5

Sequence 5. Application US/10149472

Publication No. US20040029204A1

GENERAL INFORMATION:
APPLICANT GOUBIN-GRAMATICA, FRANCOISE
APPLICANT: GOUBIN-GRAMATICA, FRANCOISE
TITLE OF INVENTION: METHOD FOR OBTAINING HUMAN CDC25 PHOSPHATASES AND METHOD
TITLE OF INVENTION: METHOD FOR OBTAINING HUMAN CDC25 PHOSPHATASE MODULATORS
TITLE OF INVENTION: MEDIES: US/10/149,472
CURRENT APPLICATION NUMBER: PR 9/15/22
FRICH RELIGING DATE: 2000-12-13
FRICH FILING DATE: 2000-12-13
FRICH FILING DATE: 2000-05-30
FRICH FILING DATE: 2000-05-30
FRICH RELIGATION NUMBER: FR 90/12008
FRICH RELIGATION NUMBER: FR 00/12008
FRICH FILING DATE: 2000-09-21
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: JM109 / PMAL - Hs Cdc25C strain
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2701 GGATCCTCCAGTCCCGGCAAGCCGCCGCGCCTGGTGGGAGG 2741
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82.0%; Score 2705.8;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2707; Conservative 0; Mismatches
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Oy 2701 GGATCCTCT 2709  Db 2701 GGATCCTCT 2709	SOLO	; TILLE REFERENCE: 612,406-033 ; CURRENT APPLICATION NUMBER: US/10/343,859 ; CURRENT FILLING DATE: 2003-11-24		; NUMBER OF SEQ ID NOS: 52 ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 8 ; LENGTH: 6648 ; TUNDE. NA	GRGANISM: Artificial sequence; PEATURE: ; GTHER: ; OTHER: ; OTHER: ; OTHER: ; TOTHER:	, % %	Gaps	Qy         1 CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60	61 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG	Db 61 GTCAATTCAGGGTGGTGAATGTGAAACCAGTAACGTTATACGATGTCGCAGAGTATGCCG 120  Qy 121 GTGTCTTATCAGACGTTTCCCGCGTGGTGAACCAGGCCAGGCCAGGTTTCTGCGAAAA 180	121	Db 181 CGCGGGAAAAAGTGGAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCAC 240	Oy 241 AACAACTGGGGGCAAACAGTCGTTGCTGATTGGCGTTGCCACTCCAGTCTGGCCTGC 300	301	301 ACGCGCCGTCGCAATTGTCGCGGCGATTAATCTCGCGCCGATCAACTGGGTGCCAGCG	Db 361 TGGTGGTGTGGTGGAACGGCGTCGAAGCCTCGAAGCGGCGGTGCAATC 420	TTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGATGACCAGGATGCCA	421	TIGGIGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGA	Oy 541 CACCCATCAACAGTATTATTTCTCCCATGAAGAGGGTACGCGACTGGGCGTGGAGCATC 600
1621 ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGAAATTCCCACAGGTT 1680 	1681 GCGGCAACTGGCGATGGCCCTGACATTATCTTCTGGGCACACGCTTTGGTGGCTAC 1740	1801 CCGITTACCTGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGATCGCTGTT 1860 	1861 GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCCGCCAAAACCTGGGAA 1920 	1921 GAGATCCCGGCGCTGGATAAAGAACTGAAAGCGAAAGGTAAGAGCGCGCTGATGTTCAAC 1980 	1981 CTGCAAGAACCGTACTTCACCTGGCCGCTGATTGCTGCTGACGGGGGTTATGCGTTCAAG 2040 	2041 TATGAAACGGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGGG 2100 	GGTCTGACCTTCCTGGTTGACCTGATTAAAAACAAACACATGAATGCAGACACCGATTAC	2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAACAAACAAAC	TCCATCGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCACGCCCGTGG	2221 GCATGGTCCAACATCGACACAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280 	AAGGGTCAACCATCCAAACCGTTCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT	2281 AAGGGTCAACCATCCAAACCGTTCGTTGGCGGGCTGCTGAGCGCAGGTATTAACGCCGCAGT 2340 2341 CCGAACAAAGAGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGATGAAGGTCTG 2400	2341 CCGAACAAAGACTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA		TTGGCGAAAGATCCACGTATTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATCATG	2461 TTGGCGAAAGATCCCACGTGTTGCCGCCACCATGGAAAACGCCCAGAAAGGTGAAATGTG 2520 2521 CCGAACATCCCGGAAGTGTCCGCTTTCTGGTATGCCGTGCGGTACTGCGGTACTGCAAGGC 2580	2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580	2581 GCCAGGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640	GCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	

1681 GCGGCAACTGGCCATGACATTATCTTCTGGGCACACGACGCTTTGGTGGCTAC 1740 	1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAGCGTTCCAGGACAAGCTGTAT 1800 1741 GCTCAATCTGGCCTGTTGGCTGAAATCACCCCGGACAAAGCGTTCCAGGACAAGCTGTAT 1800 1801 CCGTTTACCTGGGAAGCGTTAACAACGACAAAGCGTTCAATTAACTAACT	CGTTTACCTGGGGATGCCGTACGTTACAACGGCAAGCTGATTGCTTACCCGGATCGCTGTT  CBAGCGTTATACCTGGGGATGCCGTAACAACGGCAAGCTGATTGCTTACCCGGATCGCTGTT  CBAGCGTTATACCTGAATTGAAACAAAACAACAACAACAAACA	GAAGCGTTATCGCTGATTTATAACAAAGATCTGCTGCCGAACCGCCGAAAAACCTGGGAA	1921 GAGATCCCGGCGTTGGATAAGAACTGAAAGGAAAGGTAAGAGGGCGCTGATGTTCAAC 1980 		2041 TATGAAAACGCAAGTACGACATTAAAGACGTGGGCGTGGATAACGCTGGCGCGAAAGCG 2100 	2101 GGTCTGACCTTCCTGGTTGACCTGATTAAAACAACACATGAATGCAGACACCGATTAC 2160 	2161 TCCATGGCAGAAGCTGCCTTTAATAAAGGCGAAACAGCGATGACCATCAACGGCCCGTGG 2220 	2221 GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280 2221 GCATGGTCCAACATCGACACCAGCAAAGTGAATTATGGTGTAACGGTACTGCCGACCTTC 2280	2281 AAGGGTCAACCATCCAAACCGTTGGCGTGCTGAGCGCAGGTATTAACGCCGCCAGT 2340	2341 CCGAACAAAGGCTGGCAAAAGAGTTCCTCGAAAACTATCTGCTGACTGA	2401 GAAGCGGTTAATAAAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAG 2460 	2461 TIGGCGAAAGAICCACGTATIGCCGCCACCAIGGAAAACGCCCAGAAAGGTGAAAICATG 2520 	2521 CCGAACATCCCGCAGATGTCCGCTTTCTGGTATGCCGTGCGTACTGCGGTGATCAACGCC 2580 [	2581 GCCAGGGTCGTCAGACTGTCGATGAAGCCCTGAAAGACGCGCAGACTAATTCGAGCTCG 2640 	AACAACAACA            AACAACAACA	2701 GGATCCTCT 2709             2701 GGATCCTCT 2709
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TGGTCGCATTGGGTCACCAGCAAATCGCGCTGTTAGCGGGCCCCATTAAGTTCTGTCTCGG
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        US-10-343-859-9

US-10-343-859-9

Sequence 9, Application US/10343859

Publication No. US20040110161A1

GENERAL INFORMATION:
APPLICANT: Nanogen Recognomics GMBH
TITLE OF INVENTION: Method for detecting mutary TITLE OF INVENTION: Molectide sequences
FILE REPERENCE: 612,406-03

CURRENT APPLICATION NUMBER: US/10/343,859

CURRENT FILING DATE: 2003-11-24

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR PILING DATE: 2000-08-04

NUMBER OF SEQ ID NOS: 52

SOFTWARE: Patentin Ver. 2.1
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99.8%; Pred. No. 0;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
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Matches 2701; Conservative
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US-10-343-859-9
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                            APPLICANT: Abbott Laboratories
APPLICANT: Abbott Laboratories
APPLICANT: Maine, Gregory T.
APPLICANT: Patel, Chandu B.
APPLICANT: Ginsburg, Sanford R.
APPLICANT: Ginsburg, Sanford R.
TILLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TILLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REFERENCE: 6984 US. 01
CURRENT APPLICATION NUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 7112
                                                                                                                                                                                                                                                                                                     LOCATION: (1528)...(3189)
CTHER INFORMATION: pMBP-c2X-ToxoP30dell1 (52-214aa)
US-10-263-153-40
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81.5%; Score 2690.4;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2694; Conservative 0; Mismatches
Publication No. US20040067239A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Toxoplasma gondii
                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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                                    1741 GCTCAATCTGGCCTGTTGGCTGAATCACCCCGGACAAAGCGTTCCAGGACAAGCCTTAT
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1711 GCTCAATCTGGCCTGTAATCTACAACGGCAACGTCATTACTCCGGACAACGTGTTT 1860	RESULT 11 US-10-263-153-30 ; Sequence 30, Application US/10263153 ; Publication No. US20040067239A1 ; GENERAL INFORMATION: ; APPLICANT: Abbort Laboratories ; APPLICANT: Patel, Chandu B. ; APPLICANT: Patel, Chandu B. ; APPLICANT: Bliese, Timothy R.
61. CGGAACGGGAAGGCGGCGCGCGCGCGCGCATCCCCATCCAACGCGCCGCGCCGCCGCCCATCCCCCCCC	ACCGGAATTAAAGTCACCGTTGAGCATCCGGATAAACTGGAAGGAA

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TITLE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REPERENCE: 6984.08.01
CURRENT APPLICATION UNDHER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
SURBENT FILING DATE: 74
SOFFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 7259
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CCATION: (1528)...(3399)

COTHER INFORMATION: pMBP-c2X-ToxoP30dell0 (52-284aa)

MS-10-263-153-35
                                                                                                                                  ; Score 2690.4;
; Pred. No. 0;
0; Mismatches
                                                                                                                                  Query Match
Best Local Similarity 99.8%;
Matches 2694; Conservative
SEQ ID NO 35
LENGTH: 7322
TYPE: DNA
ORGANISM: TOXODlasma gondii
FEATURE:
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US-10-263-153-35
i Sequence 35. Application US/10263153
i Sequence 35. Application US/10263153
i Publication No. US20040067239A1
j GENERAL INFORMATION:
i APPLICANT: Patel, Chandu B.
APPLICANT: Patel, Chandu B.
APPLICANT: Ginsburg, Sanford R.
APPLICANT: Ginsburg, Sanford R.
APPLICANT: Ginsburg, Sanford R.
FILE OF INVENTION: GENETICALLY ENGINEERED P30 ANTIGEN,
TITLE OF INVENTION: IMPROVED ANTIGEN COCKTAIL, AND USES THEREOF
FILE REFEREENCE: 6984.US.01
CURRENT APPLICATION NUMBER: US/10/263,153
CURRENT FILING DATE: 2002-10-22
NUMBER OF SEQ ID NOS: 74
SOFTWARE: FastSEQ for Windows Version 4.0
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901 ACGATACCGAAGACAGCTCATGTTATATCCCGCCGTTAACCACCATCAAACAGGATTTTC 960	CCAATA CCAATA GGTTT	ATTAG       ATTAG TGGCG	1261 TCAGGCAGCCATCGGAAGCTGTGGTAGGCTGTGCAGGTCGTAAATCACTGCATAATTCG 1320	CTGGCAAATATTCTGAAATGAGCTGTTGACAATTAATCATCGGCTCGTATAATGTGTGGA	1441 ATTGTGAGGGGATAACAATTTCACACAGGAAACAGCCAGTCCGTTTAGGTGTTTTCACGA 1500 1501 GCACTTCACCAACAAGGACCATAGATTATGAAAACTGAAGGTAAACTGGTAATCTGG 1560	ATTAACGCGATAAAGGCTATAACGGTCTCGCTGAAGTCGGTAAGAATTCGAGAAGAT 1620 ACCGGAATTAAAGGCATCAGACGCTCCGGAAGAACGGAAGATTCCGAGAAGAT 1620 ACCGGAATTAAAAGTCACCGTGAAGCACCCGATAAACTGGAAGAGAATTCCCACAGGTT 1680 ACCGGAATTAAAGTCACCGTTGAGATCCTCGGATAAACTGGAAGAGAATTCCCACAGGTT 1680 GCGGCAACTGGCATCGCATCCTCTCTGGGCACACGACTTTGGTGGTAC 1740 GCGGCAACTGGCGATGGCCTTAATCTTCTTCTGGGCACACGGCTTTGGTGGTAC 1740 GCGGCAACTGGCGATGGCCTTAATCTTCTTCTGGGCACACGGCTTTGGTGGCTAC 1740	TGTAT 1800	MAACCTGGGAA 1920

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; OTHER INFORMATION: pMBP-c2X-ToxoP30de14C (52-294aa)  QUELY Match  Best Local Similarity 99.8%; Score 2690.4; DB 18; Length 7352;  Matches 2694; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  Matches 2694; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  CCGACACCATCGAAAGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCGGAAGAGA 60  CCGACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60  CCGACACCATCGAATGGTGAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGA 60  Qy 61 GTCAATTCAGGGTGAAAACCTTTCGCGGTATGGCATGATAGCCCCGGAAGAGA 60  CHINIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	121 GTGTCTTTATCAGCGTTTCCCGCGTGGTGAACCAGGCCAGCCA	Oy         241 AACAACTGGCGGCAAACAGTGGTTGCTGGTTGCCTCCAGTCTGGCCCTGC 300	Db   361   TGGTGGTGTGGTGGTGGTGGTGGTGGTGTGTGTGTGT	481 TIGCIGIAGGAGCACTAATGITCCGGCGTTAITTCTTGATGTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	661 GGGGTCTGGGTCTGGCTGACCAGCATAATTCTCACTGGCGGCCCATTAAGTCGCGATAG 860  Qy 661 GGGGTCTGGGTCTGGCTGGCTGAAATATCTCACTGGCAATCAAATTCAGCCGATAG 720  bb 661 GGGGTCTGGGTCTGGCTGGCTGGCTGGCATAAATTCTCACTGGCAATCAAATTCAGCGATAG 720  Qy 721 GGAACGGGAAGGCGACTGGAGTGCCATTCCACTGGCAAATGCTGA 780  721 GGAACGGGAAGGCGACTGGAGTGCCATGTCTGGTTTTCAACAAAACGTGA 780  721 CGGAACGGGAAGGCGACTGGAGTGCCATGTCTGGTTTTCAACAAAATGCTGA 780	

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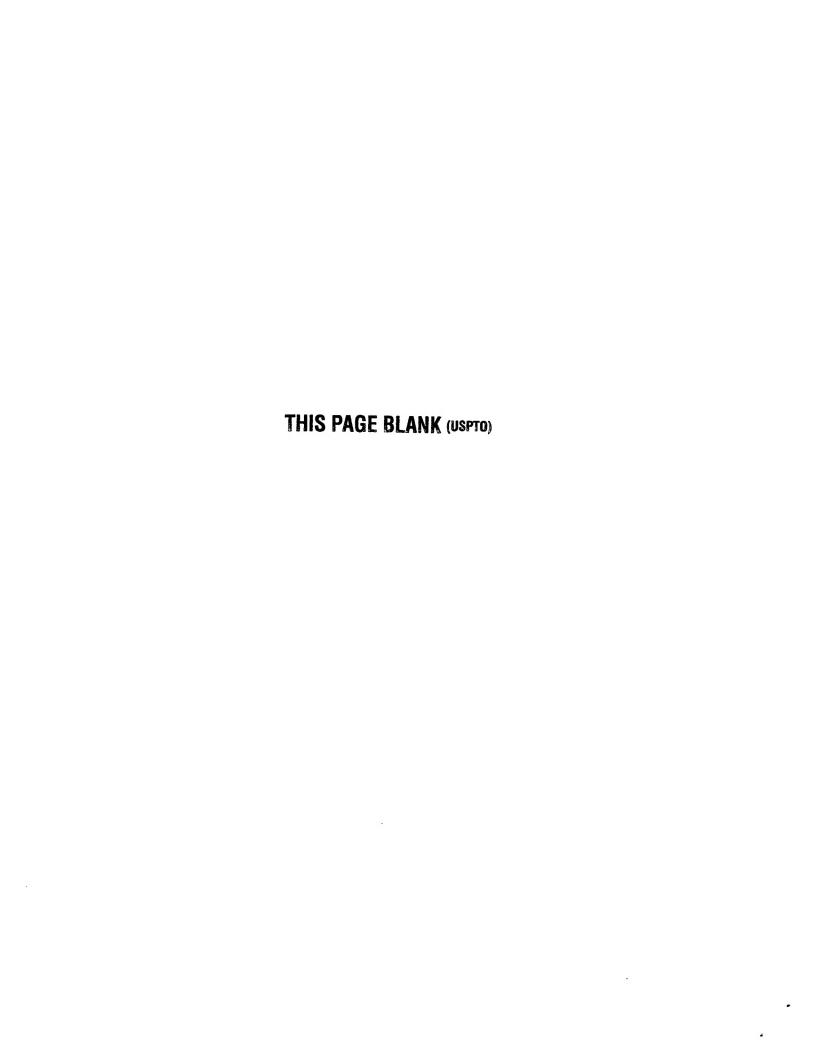
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Extraction trifolii

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Minimum DB Maximum DB

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E. coli Y1090 and phage DNA was purified from a liquid lysate. The cDNA inserts were gel purified after EcoRI digestion and ligated into pBluescript SK+. Aliquots of the ligation were used to transform E. coli DH5alpha which were plated onto medium with X-gal for selection of recombinants."
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                                                                                                                                                           GACACTTTCGAATGGCGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCCGGAAGAGAGT
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                                                                                                                  Gaps
                                                                                                                  ;
                                                                                           Length 794;
                                                                                                                  10; Indels
                                                                                         Score 778; DB 5;
Pred. No. 6e-218;
0; Mismatches 10;
                                                                                          23.6%;
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Heterodera glycines
Eukaryota; Merazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
Eukaryota; Merazoa; Nematoda; Chromadorea; Tylenchida; Tylenchida;
Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.

I (bases 1 to 779)

RS Wangux, Allen, Gao, B., Goellner, M., Maier, T., Baum, T.,
Hussey, R. and Davis, E.
Submission: Wang, Allen, Gao, Goellner, Maier, Baum, Hussey, Davis
Contact: Tom Manier
Department of Plant Pathology, Baum Lab
Iowa State University
351 Bessey Hall, Ames, IA 50011, USA
Tel: 515-294-9420
Email: trmaier@iastate.edu
Heterodera glycines Gland Cell Amplified cDNA Library, single pass
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/organism="Meterodera glycines"
/organism="MRNA"
/db xref="taxon:51029"
/cell type="gland"
/dev stage="mixed parasitic juvenile"
/clone lib="Gland Cell Amplified cDNA Library"
/note="Organ: gland cell; Vector: pSportII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 779;
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Pred. No. 9.3e-216;
0; Mismatches 5;
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CK394523
CK394523.1 GI:40389794
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Best Local Similarity 99.4%;
Matches 773; Conservative
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RESULT

CK394523 779 bp mRNA linear EST 30-DEC-2003 hggada4D08 Gland Cell Amplified cDNA Library Heterodera glycines

m

746 180

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989

/Lissue\_Type="inflorescence meristem"
/(issue\_Type="inflorescence meristem"
/dev\_stage="about one week after bolting"
//deb\_note="E. coli SCS-1/pSB111"
/(clone\_lib="AtM")
/(clone\_lib="AtM")
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23.3%; Score 768; DB 7; Length 769; 100.0%; Pred. No. 5.4e-215; Best Local Similarity

Query Match

ORIGIN

1044 1104 BQ751655 793 bp mRNA linear EST 18-JUL-2002 EST632218 DSCT Colletotrichum trifolii cDNA clone pDSCT6-59, mRNA sequence. ö 540 9 99 564 180 624 240 300 744 360 804 420 864 480 924 984 684 9 Collectrichum trifolii
Collectrichum trifolii
Collectrichum trifolii
Collectrichum trifolii
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
mitosporic Phyllachoraceae; Collectrichum.
1 (bases 1 to 793)
Samac, D.A., Dickman,M., Town,C.D., Van Aken,S., Utterback,T.,
Cheung,F. and Fraser,C.M.
ESTS from mycelia of Colletotrichum trifolii race 1
Unpublished (2002) CACTGGTAAAAGAAAACCCCCGGGGCCCAATACGCAAACCGCCTCTCCCCGGGCT 121 ATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTCT CCCATGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAA 181 cccargaagacggracgcgacrgggggggggggggcarcrggracgarcaccaagaa TGCTGGTTGCCAACGATCAGATGGCGCTGGGCCGCAATGCGCGCCATTACCGAGTCCGGGC 481 TGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGACGACGATACCGAAGACAGCTCATGTT 541 ATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGGAAACCAGCGTGG ACCECTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCT 661 CACTGGTGAAAAGAAAACCACCTGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGT GCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGC GCGGCGTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGC ATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCCATCAACAGTATTATTTCT ATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTG CCATGTCCGGTTTTCAACAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGA TGCTGGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCCATTACCGAGTCCGGGC 865 TGCGCGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTT ATATCCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCAGCGTGG Gaps ö Indels .. Mismatches ; 0 GI:21907060 Conservative BQ751655 BQ751655.1 768; 925 985 601 1045 1105 805 385 265 685 361 421 505 625 745 RESULT 4 BQ751655 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL REFERENCE AUTHORS Matches 셤 ρp g g 엄 ò g 8 g ð g ઠ 셤 ò ò ò 엄 à 8 ò 8 g à

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Colletotrichum trifolii

Colletotrichum trifolii

Edwaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes in Ascomycota; Phyllachorales;
Sordariomycetes; Phyllachoraceae;
Sordariomycetes; Phyllachoraceae;
I (bases I to 806)

E (bases I to 806)

Samac, D.A., Dickman, M., Town, C.D., Van Aken, S., Utterback, T.,
Cheung, F. and Fraser, C.M.

ETST from mycelia of Colletotrichum trifolii race I

Unpublished (2002)

Contact: Deborah A. Samac

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495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA

Tel: 612 645 51243

Fax: 616 649 5058
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EST631783 DSCT Colletotrichum trifolii cDNA clone pDSCT3-64, mRNA
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Stratagene and packaged using Gigapack packaging extracts.
An aliquot of the amplified library was used to transduce
E. coli Y1090 and phage DNA was purified from a liquid
                                                                                                                                                                                                                        CGTCTGCGTCTGGCTGGCATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCG 722
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TIGR sequence name: MTSAC64TV More information is available at:
www.medicago.org
Seq primer: (gtA AtA CGA CtC ACt AtA ggg C).
              GCTGTGGAAGCTGCCTGCACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACA
                                                                                                   CCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGCGGCGTGGAGCATCTG
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enriched RNA The cDNA was ligated into Lambda gill from
Stratagene and packaged using Gigapack packaging extracts
An aliquot of the amplified library was used to transduce
E. coll Y109 and phage DNA was purified from a liquid
lysate. The cDNA inserts were gel purified after EcoRI
digestion and ligated into pBluescript SK+. Aliquots of
the ligation were used to transform E. coli DH5alpha which
were plated onto medium with X-gal for selection of
                                                                                               Paul, MN 55108, USA
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              Contact: Deborah A. Samac
Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 551
Tel: 612 625 1243
Fax: 651 649 5058
Email: debbys@puccini.crl.umn.edu
TIGR sequence name: MTSAF59TV More information is available
www.medicago.org
Seq primer: (gtA AtA CgA CtC AtA ggg C).
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                                                                                                                                               GACACTITICGAATGGCGCAAAAACCTITICGCGGTATGGCGTGATAGCGCCCGGAAGAGAGGT
                                                                                                                                                                                             CAATTCAGGGTGGAATGTGAAAACCAGTAAACGTTATACGATGTCGCAGAGTATGCCGGT
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                                                                                                                                 GACACCATCGAATGGTGCAAAACCTTTCGCGGTATGGCATGATAGCGCCCGGAAGAGAGT
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                                                                                                            Gaps
                                                                                                         2;
                                                                                  Length 806;
                                                                                                          16; Indels
                                                                                 22.9%; Score 755.4; DB 5; ilarity 97.4%; Pred. No. 2.9e-211; Conservative 0; Mismatches 16;
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CB863541 689 bp mRNA linear EST 22-APR-2003 HH04A08y HH Hordeum vulgare cDNA clone HH04A08 3-PRIME, mRNA sequence.

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                                                                Hordeum vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Hordeum.
1 (baees 1 to 689)
Varshney, R.K.; Zhang, H., Burton, R., Stein, N., Langridge, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /notes="Vector: psport; Site_1: SalI (5-end of cDNA);
Site_2: NotI (3-end of cDNA); Due to the cloning system
used blue/white selection for recombinants is not 100 i
reliable. Average insert size is 1.3 kb."
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                                                                                                                                                                                                                                                                                 Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Sloop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="coleoptile"
/dev_stage="coleoptile, 1
/lab_host="DH10B"
                                                                                                                                                                                                                                Barley ESTs from coleoptile tissue Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                        Email: stein@ipk-gatersleben.de
Insert Length: 689 Std Error:
Plate: 4 row: A column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GABI:555198"
/db_xref="taxon:4513"
/clone="HH04A08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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GI:30058100
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                                              Hordeum vulgare
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AY080106 AY080106 Scripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3G6L, genomic survey
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                                                                                                GCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAGTCGTTGCTGAT 271
                                                                                                                                                                                              AATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGGTCGATGGTAGAACGAAGCGGCG 390
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uncultured marine virus
furuses, environmental samples.

(Dases 1 to 710)
Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M.,
Mead, D., Azam, F. and Rohwer, F.
Seconcic analysis of uncultured marine viral communities
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
                                                                                                                                                                                                                                                                 272 TGGCGTTGCCACTCCAGTCTGGCCCTGCAC-GCGCCGTCGCAAATTGTCGCGGCGATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCAGGCCAGCCACGTTTCTGCGAAAACGCGGG-AAAAAGTGGAAGCGGCGATGGCGGA
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Biology Dept.
Balology State University
San Diego State University
S500 Campanile Dr. San Diego, CA 92102, US.
Tel: 6195941336
Fax: 619595576
Fmail: forest@sunstroke.sdsu.edu
Class: shotgun.
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DKFZp566E0346_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFZp566E0346_s', mRNA sequence.
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
emails consortium of the German Genome Project. No s1 sequence
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1 (bases 1 to 712)
Ottenwaelder, B., Obermaier, B., Mewes, H.W., Gassenhuber, J. and
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                                                                                                                                   209 ACTAATGITCCGGCGTIATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATT
                                                                                                                                                                                                                                         TTCTCCCATGAAGACGGTACGCGACTGGAGCATCTGGTCGCATTGGGTCACCAG
                                                                                                                                                                                                                                                                                                                                                       89 CAAATCGCGCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGCGTCTGCGTCTGGCT
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                                                                                                      ACTAATGTTCCGGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATT
33 GGTATGGCATGATAGCGCCCGGAAGAGAGTCAATTCAGGGTGGTGAATGTGAAACCAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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/mol_type="mRNA"
/dolone="bkzp56620346"
/tissue_type="kidney"
/dov_etage="fetal"
/lab_host="X1-2blue"
/clone_lib="566 (synonym: hfkd2)"
/note="Vector: pAMP1; Site_1: Not1; Site_2: SalI"
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99.6%; Pred. No. 6.4e-188;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                TGGCATAAATATCTCACTCGCAATCAAAT 709
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Unpublished (1999)
Contact: MIPS
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Best Local Similarity 99.6'
Matches 699; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 660)
                                                                                                                                                                                                                                                                                                                                      Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No rl sequence available.
This clone (DKRZp434102) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GRRMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145 GCGTGGTGAACCAGGCCAGCCATTTCTGCGAAAAACGCGGGAAAAAGTGGAAGCGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 GCGTGGTGAACCAGGCCAGCCACGTTTCTGCGAAAAACGCGGGAAAAAAAGGGGGAAAGCGGCGA
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  clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="Vector: pSport1; Site_1: Not1; Site_2: SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
DKFZp434I102_s1 434 (synonym: htes3) Homo sapiens cDNA DKFZp434I102_3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.6%; Score 647.4; DB 1; Length 660; 99.7%; Pred. No. 2.4e-179; Live 0; Mismatches 1; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="testis"
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/lab_host="DH108"
/clone_lib="434 (synonym: htes3)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mol_type="mRNA"
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Unpublished (1999)
Contact: MIPS
                                         AL044483
AL044483.1 GI:5432701
EST.
                                                                                                       Homo sapiens (human)
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Matches 659; Conservative
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                                                                                   /note="Marine viruses were isolated from 200 liters of surface seawater using a combination of differential filtration and density-dependent gradient centrifugation. Linker-amplified shotgun libraries were constructed by randomly shearing the total marine viral community DNA, end-repairing, ligating dsDNA linkers to the ends, and amplifying the fragments using Vent DNA polymerase. The resulting fragments were ligated into the pSMART vector and electroporated into MC12 cells (Lucigen; Middleton, W1)"
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                                         /clone="S1051p3G6L"
/clone_lib="Scripps Pier (La Jolla, CA) uncultured virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 AACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCTGGTTGCCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 ATCAGATGGCGCTGGGCGCAATGCGCGCCATTACCGAGTCCGGGCTGCGCGTTGGTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATATCTCGGTAGTGGGATACGACGATACCGAGGCTCATGTTATATCCCGCCGTTAA
                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                            Score 676; DB 8; Length 710;
Pred. No. 8.4e-188;
0; Mismatches 7; Indels
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mol_type="genomic DNA"
db_xref="taxon:186617"
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                                                                                                                                                                                                                                                                                                                                                              20.5%;
98.9%;
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Best Local Similarity 98.9
Matches 690; Conservative
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CB863814 62-APR-2003
HH07B20y HH Hordeum vulgare cDNA clone HH07B20 3-PRIME, mRNA
                                                                                                                           329
         461 GAGCTGAATTACATTCCCAACCGCGTGGCACACAACTGGCGGGGCAACAGTCGTTGCTG 402
                                                                                                                                                                                                                                                449
                                                                                                                                                                                                                                                           509
                                                                                                                                                                                                                                                                                                                                                                      569
                                                                                                                                                                                                                                                                                                                                                                                                   102
                                                                                                                                                                                                                                                                                                                                                                                                                         570 GAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATCGCG 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare
Hordeum vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 624)
Varshney,R.K., Zhang,H., Burton,R., Stein,N., Langridge,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                           210 GAGCTGAATTACATTCCCAACCGCGTGGCACAACAACTGGCGGGCAAACAATCGTTGCTG
                                                                                                                   270 ATTGGCGTTGCCACTCCAGTCTGGCCCTGCACGCGCCGTCGCAAATTGTCGCGGGGATT
                                                                                                                                    GTCGAAGCCTGTAAAGCGGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATC
                                                                                                                                                                                                                                                                                                                                510 CCGCGTTATTTCTTGATGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCAT
                                                                                                                                                                            330 AAATCTCGCGCCGATCAACTGGGTGCCAGCGTGGTGGTGTCGATGGTAGAAGCGGC
                                                                                                                                                                                                                                                                                                     Barley Ests from coleoptile tissue
Unpublished (2003)
Unpublished (2003)
Unpublished (2003)
Ontact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Correspect: 3, 06466, Gatersleben, Germany
Tel: 039482-5592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mixth" |
/cultivar="$10op" |
/db_xxef="GAB1:555471" |
/db_xref="taxon:4513" |
/clone="HH07B20" |
/tissue_type="coleoptile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: stein@ipk-gatersleben.de
Insert Length: 624 Std Error:
Plate: 7 row: B column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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CB863814.1 GI:30058373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence.
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AUTHORS
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624
                                                              625 recectorinage de contra diretere recese de concrete en en 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Ambibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Kenopous, Kenopous, Kenopous, I (bases 1 to 641)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 GTGAACCAGGCCAGCCACGTTTCTGCGAAAACGCGGGAAAAAGTGGAAAGCGGCGATGGCG 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL.
                                            CCCATGAAGACGGTACGCGACTGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAA
                                                                                                                         685 ATAAATATCTCACTCGCAATCAAATTCAGCCGATAGCGGGAACGGCGACTGGAGTG
                                                                                                                                                                                    61 ATAMATATCTCACTCGCAATCAACTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGGTATGGCATGATAGCGCCCCGGAAGAGAGTCAATTCAGGGTGGAATGTGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.4%; Score 641; DB 4; Length 64 clarity 100.0%; Pred. No. 1.8e-177; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed genes in X. laevis embryo
Unpublished (2001)
Contect: Tadasu Shin-i
Contect: Tadasu Shin-i
Contect For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://xenopus.nibb.ac.jp.
Location/Qualifiers
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BJ063872.1 GI:17471074
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nes 641, Conservat
                                                                                                                                                                                                                              745 C 745
                240
                                              565
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Best Local S:
Matches 641
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VERSION
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ORGANISM
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BJ063872/c
                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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                                                               Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 3' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Sequencing consortium of the German Genome Project. rl sequence
also available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTGTTAGCGGGCCCATTAAGTTCTGTCTCGGCGCGTCTG-GTCTGGCTGGCTGGCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              436 CCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGGAAACCAGCGTGGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGCCAATCAGCTGTTGCCCGTCTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 CGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGAGACGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGAAGACGGTACGCGACTGGGCGTGGAG-ATCTGGTCGCATTGGGTCACCACCACAAATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATCTCACTCGCAATCAAATTCAGCCGATAGCGGAACGGGAAGGCGACTGGAGTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCCATTACCGAGTCCGGGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTGCCAACGATCAGATGGCGCTGGGCGCAATGCGCGCCCATTACCGAGTCCGGGCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTGGTGCGGATATCTCGGTAGTGGGATACGACGATACCGAAGACAGCTCATGTTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCGCCGTTAACCACCATCAAACAGGATTTTCGCCTGCTGGGGCAAACCAGCGTGGACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 CTTGCTGCAACTCTCTCAGGGCCAGGCGGTGAAGGGCAATCAGCTGTTGCCCGTCTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGTGAAAAGAAAAACCACCCTGGCGCCCCAATACGCAAAACCGCCTCTCCCCCGCGCGTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 GGTGAAAAGAAAACCACCCTGGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGATTCATTAATGCAGCTGGCACGACAGGTTTCCCCGACTGGAAAGCGGGCAGTGAGCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAAGACGGTACGCGACTGGGCGTGGAGCATCTGGTCGCATTGGGTCACCAGCAAATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCCGGTTTTCAACAAACCATGCAAATGCTGAATGAGGGCATCGTTCCCACTGCGATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                 /dev_stage="addlt"
/lab_host="DH10B"
/clone_lib="434 (synonym: htes3)"
/note="Vector: pSport1; Site_1: Not1; Site_2: Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.5%; Score 612; DB 1; Length 79
99.7%; Pred. No. 7.3e-169;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCCAATTAATGTGAGTTAGCTCACTCATTAGGCAC 1204
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                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZ04348075"
/tissue_type="testis"
   et al.)
 EST (Duesterhoeft,
Unpublished (1999)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity 99.7
634; Conservative
                                                                                                                                                                                                                                                1. .794
                                                      MIPS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 794)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
/dev_stage="coleoptile, 1 day old"
/lab.host="DH108"
/clone lib="HH"
/note="Vector: pSPORT; Site_1: SalI (5-end of cDNA);
Site_2: NotI (3-end of cDNA); Due to the cloning system used blue-white selection for recombinants is not 100 % reliable. Average insert size is 1:3 kb."
                                                                                                                                                                                                                                                                                                                                                                     CGGGAAAAAGTGGAAAGCGGCGATGGCGGAGCTGAATTACATTCCCAACCGCGTGGCACAA
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DKFZp434B075_81 434 (synonym: htem3) Homo sapiens cDNA clone
                                                                                                                                                                                           ;
                                                                                                                                                           6; Length 624;
                                                                                                                                                                                           Indels
                                                                                                                                                       18.7%; Score 615.8; DB 6; 99.7%; Pred. No. 5.1e-170; tive 0; Mismatches 2;
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Matches 617; Conservative
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KEYWORDS
SOURCE
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2414 AAGACAAACCGCTGGGTGCCGTAGCGCTGAAGTCTTACGAGGAAGAGTTGGCGAAAGATC 2473
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                                                                                                                                                                                                           2594 AGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT 2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Rohwer F
Biology Dept.
Baology Dept.
San Diego State University
5500 Campanile Dr. San Diego, CA 92102, US.
Tel: 6195941336
Fax: 6195955676
Fmail: forest@sunstroke.sdsu.edu
Class: shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
17.9%; Score 589.8; DB 8;
Best Local Similarity 99.7%; Pred. No. 2.5e-162;
Matches 591; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                   AGACTGTCGATGAAGCCCTGAAAGACGCGCAGACT 118
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PR10124a_C01 - PR10124a.B21 (752) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
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Pristionchus pacificus
Bukaryota, Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 752)
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Appabls en AcedB database for the nematode satellite organism
Pristionchus pacificata
Nucleic Acids Res. 32 (1), D421-D422 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1996 ITCACCTGGCCGCTGATTGCTGCTGAC-GGGGGTTATGCGTTCAAGTATGAAAACGGCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           end
                                                                                                                                                                                                                                                                                                                                           Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601371
Email: ralf. sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and sequenced at Vancouver, Canada.
Class: fogmid ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
18.3%; Score 603; DB 9; L
Best Local Similarity 98.9%; Pred. No. 3.3e-166;
Matches 628; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="taxon:54126"
                                                                                                                            CL655575.1 GI:50134897
                                                                                           survey sequence.
CL655575
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 RESULT 13
CL655575/c
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ORGANISM
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VERSION
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Viruses; environmental samples.

1 (bases; environmental samples.

Breitbart, M., Salamon, P., Andresen, B., Mahaffy, J.M., Segall, A.M., Mead, D., Azam, F. and Rohwer, F.

Benomic analysis of uncultured marine viral communities
Proc. Natl. Acad. Sci. U.S.A. 99 (22), 14250-14255 (2002)
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/mol_type="genomic DNA"
/db xref="taxon:186617"
/clone="$IO51p3D4L"
/clone lib="Scripps Pier (La Jolla, CA) uncultured virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY080094 Aripps Pier (La Jolla, CA) uncultured virus community uncultured marine virus genomic clone SIO51p3D4L, genomic survey
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Emails wiemann@dkfz-heidelberg.de;
sequenced by GBF (National Research Centre for Biotechnology Ltd
Braunschweig/Germany) within the cDNA sequencing consortium of
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No all sequence available.

This clone (DKEZp564C157) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
AAGTICTGTCTCGGCGCGTCTGCGTCTGGCTGGCTGGCATAAATATCTCACTCGCAATCA
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Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Gassenhuber, J.
                                                                      GGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCGCTGGA
                                                                                                                           TGTCTCTGACCAGACACCCATCAACAGTATTATTTTCTCCCATGAAGACGGTACGGACT
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                                                        GGCGGTGCACAATCTTCTCGCGCAACGCGTCAGTGGGCTGATCATTAACTATCCGCTGGA
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/organism="Homo sapiens"
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Unpublished (1999)
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                                                                                                                                                                       Gaps
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/clone_lib="564 (synonym: hfbr2)"
/note="Vector: pAMPl; Site_1: NotI; Site_2: SalI"
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Job time : 6745.2 secs
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